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OM nucleic - nucleic search, using sw model

Run on: January 14, 2005 21:22:35 ; Search time 11079 Seconds

(without alignments) 11435.067 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagaattcgccgagcgccg.....acaaaaaaaaaaaaaaaaa 2679

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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5: gb_ov:*
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9: gb_pr:*
10: gb_ro:*
11: gb_ses:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2679	100.0	2679	9 AF170724	Homo sapi
2	2566.4	95.8	2639	9 AX877194	Sequence
3	2566.4	95.8	2639	6 BD156534	Primer fo
4	2566.4	95.8	2639	9 AK027687	Homo sapi
5	2497.2	93.2	3189	9 BC012072	Homo sapi
6	2262.4	84.4	3138	6 AX877222	Sequence
7	2262.4	84.4	3138	6 BD156548	Primer fo
8	2262.4	84.4	3138	9 AK001658	Homo sapi
9	2244.6	83.8	3181	6 AX405642	Sequence
10	1919.4	71.6	2448	6 AX834949	Sequence
11	1919.4	71.6	2448	9 AK097671	Homo sapi
12	1491	55.7	3194	10 BC049792	Mus muscu
13	1279.8	47.8	6235	6 BD183291	Novel gen
14	961.8	35.9	2257	9 AK090948	Homo sapi
15	876.2	32.7	2186	6 AX713476	Sequence
16	876.2	32.7	2186	9 AK054917	Homo sapi
17	727	27.1	816	6 AX868758	Sequence
18	727	27.1	816	6 BD148820	Primer fo
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22	608.4	22.7	181438	2 AC023047	Homo sapi
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26	488.8	18.2	518	6 BD153851	Primer fo
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28	440.8	16.5	273812	2 AC106441	Rattus no
29	430.4	16.1	236751	2 AC128407	Rattus no
30	416	15.5	61779	2 AC126301	Rattus no
31	218	8.1	181438	2 AC023047	Homo sapi
32	142.4	5.3	202792	2 AC125898	Rattus no
33	139.2	5.2	158697	2 AC118260	Mus muscu
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37	85.2	3.2	338116	2 AC087159	Mus muscu
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ALIGNMENTS

RESULT 1
AF170724
LOCUS AF170724
DEFINITION Homo sapiens cell cycle checkpoint protein CHFR mRNA, complete cds.
ACCESSION AF170724
VERSION AF170724.1 GI:9651169
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Scolnick, D.M. and Halazonetis, T.D.
TITLE Chfr defines a mitotic stress checkpoint that delays entry into metaphase
JOURNAL Nature 406 (6794), 430-435 (2000)
MEDLINE 20388685
PUBMED 10935642
REFERENCE
AUTHORS Halazonetis, T.D. and Scolnick, D.M.
TITLE Direct Submision
JOURNAL Submitted (21-JUN-1999) Wistar Institute, 3601 Spruce Street, Philadelphia, PA 19104, USA
FEATURES
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/db_xref="taxon:9606"
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 AX877194 2639 bp DNA linear PART 17-DEC-2003
 LOCUS AX877194 Sequence 12099 from Patent EP1074617.
 DEFINITION AX877194
 ACCESSION AX877194
 VERSION AX877194.1 GI:40031930
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS 1
 TITLE Oda, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., and Otsuki, T.
 JOURNAL Primers for synthesizing full-length cDNA and their use
 Patent: EP 1074617-A 12099 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES
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 /note="unassigned protein product"
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 /db_xref="GI:40031931"
 /translation="MERPEEGKQSPPEQWGRLLRLGAEBSGPHVLLRKREWTIGRRR

ORIGIN

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 QY 17 GCCGCAATGCTCTTGAACAGCGCGCGCGAGCGGTTCCGGGTTCCGGCGCGGCGG 76
 DB 5 GCCGCAATGCTCTTGAACAGCGCGCGCGAGCGGTTCCGGGTTCCGGCGCGGCGG 64
 QY 77 GATGTAATCCCGATGAGCGCGCCGAGAGAGCAGAGTCCCGCGCGCGAGCCT 136
 DB 65 GATGTAATCCCGATGAGCGCGCGCCGAGAGAGCAGAGTCCCGCGCGCGAGCCT 124
 QY 137 GGGGACGGCTCTGCTGCTGGCGCGGAGAGGCGGAGCGGCGGCGGCGGCGGAGC 196
 DB 125 GGGGACGGCTCTGCTGCTGGCGCGGAGAGGCGGAGCGGCGGCGGCGGCGGAGC 184
 QY 197 GGGAGTGAACATCGGCGCGAGAGAGTGGAGCTTCTTCCCGACATTAACCTG 256
 DB 185 GGGAGTGAACATCGGCGCGAGAGAGTGGAGCTTCTTCCCGACATTAACCTG 244
 QY 257 TCTTGGAGATCATGTGAATTTGATGATGAATAATCAGGTGAGTGAACCTGAG 316
 DB 245 TCTTGGAGATCATGTGAATTTGATGATGAATAATCAGGTGAGTGAACCTGAG 304
 QY 317 ATACGAGACAGGTGAACAGATTAACAGCTGAAGTTTGAAGAGCAGATGCG 376
 DB 305 ATACGAGACAGGTGAACAGATTAACAGCTGAAGTTTGAAGAGCAGATGCG 364
 QY 377 CTTTACAGCTGGGATGTCATCTTGTGTAAGAGATGAACCGAGAACACAG 436
 DB 365 CTTTACAGCTGGGATGTCATCTTGTGTAAGAGATGAACCGAGAACACAG 424
 QY 437 TGGCATACCTTATGAATCTTTAAGTGAAGCAAGCATGACACAGATCTTTGAAG 496
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 QY 497 CTAAACAGAAATGTGTTCCATGGGACCAAGATTAACCTCAGGTGAGTGAAGGCGAG 556
 DB 481 -----GATTAACCTCAGGTGAGTGAAGGCGAG 508
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 QY 1037 GTTTGAGAGCCCTGAG 1096
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 DB 2249 TGGTGAAGGCTGGGCGAGGCTCGT 2308
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 DB 2429 ACATTTTGTGAG 2488
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 LOCUS 2639 bp DNA linear PAT 17-JAN-2003
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD156534.1 GI:27862292
 VERSION JP 2002191363-A/11377.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2639)
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002191363-A 11377 09-JUL-2002;
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/11377
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990

QY 1877 GAGACACCGTTCTGTGTACTGTCTGTGCGCTTCCGTGAGCTGACCTATCACT 1936
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 DB 2609 TTGACAAAAA 2618
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 DEFINITION to TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.
 AK027687
 VERSION AK027687.1 GI:14042552
 KEYWORDS Oligo cloning; fls (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
 Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
 Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,

Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
 Nagahari, K., Murakami, K., Yasuda, T., Iwyanagi, T., Nagatsuna, M.,
 Shiratori, A., Sudo, H., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
 Kikawa, E., Omura, Y., Abe, K., Kanbara, K., Katsuta, N., Sato, K.,
 Tanikawa, M., Yamazaki, M., Nimomiya, K., Ishibashi, T., Yamashita, H.,
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 Hirooka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
 Yosida, M., Hottuta, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A.,
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 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
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 Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
 Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsunura, K.,
 Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
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 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
 Nagase, T., Nomura, N., Kikuchi, H., Masuno, Y., Yamashita, R.,
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length
 human cDNAs
 Nat. Genet. 36 (1), 40-45 (2004)
 14702039
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 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Aotsuka, S., Yoshikawa, Y.,
 Matsunawa, H., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,
 Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuno, Y. and Sasaki, N.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 2639)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
 (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction,
 5' - & 3' end one pass sequencing and clone selection; Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.
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RESULT 5
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DEFINITION Homo sapiens checkpoint with forkhead and ring finger domains, mRNA
ACCESSION BC012072
VERSION   BC012072.1
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens (human)
REFERENCE
AUTHORS   Rukerlyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 3189)
          Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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          Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
          Scherch, A., Schein, J.E., Jones, S.J. and Marr, M.A.
          Generation and initial analysis of more than 15,000 full-length
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          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          22388257
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          12477932
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          2 (bases 1 to 3189)
          Strausberg, R.
          Direct Submission
          Submitted (02-AUG-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
          NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
          Info@cgsc.bc.ca
          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butlerfield,
          Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
          Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
          Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
          Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
          Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,
          Michael Thorpe, Miranda Tsai, Natafja van den Bosch, Jill Vardy,
          George Yang, Scott Zuyderduyn, Marco Marra.
          Clone distribution: MGC clone distribution information can be found
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 Matches 2545; Conservative 0; Mismatches 3; Indels 36; Gaps 1;

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DEFINITION Sequence 12127 from Patent EP1074617.
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VERSION AX877222.1 GI:40031958
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 Ota, T., Iwaga, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: JP 1074617-A 12127 07-FEB-2001;
Research Association for Biotechnology (JP)
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Db 1 CTCTTGAAG 60

Qy 87 CCCGATGAG 146

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 ACCESSION AX405642
 VERSION AX405642.1 GI:21438723
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 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Tang, Y. T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q. A., Ren, F.,
 TITLE Xue, A. J., Yang, Y., Wehrman, T. and Drmanac, R. T.
 JOURNAL Novel nucleic acids and polypeptides
 Patent: WO 0222660-A 57 21-MAR-2002;
 HSEQ, INC. (US)
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ORIGIN

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 Best Local Similarity 92.3%; Pred. No. 0;
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LOCUS DEFINITION
AX834949 Sequence 2073 from Patent EP1347046.
ACCESSION
VERSION AX834949.1 GI:39921084
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuko,Y.

TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 2073 24-SEP-2003;
FEATURES Research Association for Biotechnology (JP)
source location/Qualifiers
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ORIGIN
Query Match 71.6%; Score 1919.4; DB 6; Length 2448;
Best Local Similarity 88.5%; Pred. No. 0;

Matches 2227; Conservative 0; Mismatches 6; Indels 284; Gaps 2;

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				AK097671.1	GI:21757518		
						oligo capping, f18 (full insert sequence).	
						Homo sapiens (human)	

REFERENCE
AUTHORS
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,

1enai, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
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Okajima, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shimai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagaie, T., Shimura, N., Kikuchi, H., Masuo, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,

TITLE NED0 human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 2448)
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HHI Team) ; 2-6-7

COMMENT
NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - 3' and one pass sequencing: RAB, HRI, and Biotechnology Center; National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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 DEFINITION Mus musculus checkpoint with forkhead and ring finger domains, mRNA
 ACCESSION BC049792
 VERSION BC049792.1 GI:29437110
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Db      1927  CATTCCTGCTTGTGAGTTGCGAGTGCAGTGCAGTCAATCCGCTCTGACTGTGAGGCG 1986
Qy      2007  TAACTGCGCACTCAGTGAAGAGCTCACCAAGCATGAATTAATCAATATCTGTGAACA 2066
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ACCESSION    BD183291
VERSION      BD183291.1 GI:31875491
KEYWORDS     JP 2002345492-A/4.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 6235)
AUTHORS      Ohara, O., Nagase, T. and Nakajima, D.
TITLE        Novel genes and proteins encoded by the genes

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JOURNAL Patent: JP 2002345492-A 4 03-DEC-2002;
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 PN JP 2002345492-A/4
 PD 03-DEC-2002
 PE 26-FEB-2002 JP 2002049009
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 PC C12N15/09, C07K14/47//A61K31/711, A61K38/00, A61K48/00, A61P25/00,
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 QY 1414 CCCCATGCGCCAGACCCGAGGGGCGAGCGAGAGCCGACAGCGCTGGGGGATGACACC 1473
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 AK090948
 VERSION AK090948.1 GI:21749208
 ACCESSION
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabara, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Send, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Saitoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuko, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

2
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuko, Y., Nagai, K. and Isogai, T. NEBO human cDNA sequencing project
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
3 (bases 1 to 2257)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FUJ Project (HRI Team) ; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genominfo@ri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) ; cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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ORIGIN
source

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Db 1629 TAAA 1633

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LOCUS AXT13476
DEFINITION Sequence 160 from Patent EP1293569.
ACCESSION AXT13476
VERSION AXT13476.1 GI:29888332
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuko, Y. Full-length cDNAs
Patent: EP 1293569-A 160 19-MAR-2003;
Helix Research Institute (JP) ; Research Association for Biotechnology (JP)
Location/Qualifiers
1. 2186
/organism="Homo sapiens"

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
Full-length cDNAs
Patent: EP 1293569-A 160 19-MAR-2003;
Helix Research Institute (JP) ; Research Association for Biotechnology (JP)
Location/Qualifiers
1. 2186
/organism="Homo sapiens"

ORIGIN

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.7%; Score 876.2; DB 6; Length 2186;
Best Local Similarity 99.4%; Pred. No. 1.1e-191;
Matches 890; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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QY 1832 CTCTCAGGGGGAGAGTTTCTGCTGTGATTAACAGTCAAGGAGACACCGTTCTGT 1891
DB 731 CTCTCAGGGGGAGAGTTTCTGCTGTGATTAACAGTCAAGGAGACACCGTTCTGT 790
QY 1892 GTTACTGCTGTGGCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATGGGAGAAATTC 1951
DB 791 GTTACTGCTGTGGCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATGGGAGAAATTC 850
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DB 851 CTGCTTCCGAGTTGCCAGTGGCCGTAAACATCCCGTCTGACTGTGAGGCGGTAACT 910
QY 2012 GCCGCACTAGGTAAGCTCAACGCGCATGAAATTCATATCTGTGAACAGACAA 2071
DB 911 GCCGCACTAGGTAAGCTCAACGCGCATGAAATTCATATCTGTGAACAGACAA 970
QY 2072 GGTCAAAAACCTAAGCATCCAGAGCCCTGAGCAGCTTCAAGCTGAGGTGAAGAG 2131
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DB 1031 CGTGTTTTAAATACAGACAGACAGTCAAGGTGTTTCAAGCCCTGAGGAG 1090
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QY 2252 GAGTGAACCTCCCGAGAGCCCGGGGGCCGAGCCGCTCTGTGAGCGCTGGGC 2311
DB 1149 GAGTGAACCTCCCGAGAGCCCGGGGGCCGAGCCGCTCTGTGAGCGCTGGGC 1208
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DB 1509 ATGTCAAAACTGTAGCACAATAATATATTTAATTTTACAAATGACAAAA 1563

Search completed: January 15, 2005, 04:02:36
Job time : 11105 secs

1. **Introduction**

XX The present sequence is that of cDNA encoding the human mitotic
CC checkpoint protein Chfr (see AAB20219) having a forkhead associated
CC domain (FHA) and a ring finger domain. The protein is required for
CC regulation of the transition of cells from prophase to metaphase during
CC mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint
CC was evident in primary human cells, but was inactivated in 4 of 8 human
CC cancer cell lines. In U2OS cells, a mutation was identified, which caused
CC a Val to Met amino acid substitution in the highly conserved C-terminal
CC Cys-rich region of the Chfr protein. In the absence of the Chfr
CC checkpoint, cells subjected to mitotic stress condensed their chromosomes
CC despite failing to separate their chromosomes. Chfr may monitor
CC centrosome separation. Inactivation of the Chfr gene in human cancer is
CC theorized to underlie the increased sensitivity of cancer cells to
CC antimetabolic drugs. Nucleic acids comprising the present sequence, or
CC sequences encoding at least amino acids 31-103, 303-346, 476-641 (or
CC their antisense sequences) are claimed. The Chfr cDNA was isolated from
CC an expressed sequence tag database sequence for cDNAs with FHA motifs.
CC Claimed methods of determining the tumorigenic potential of a cell
CC comprise examining the cell for the presence of Chfr nucleic acid
CC (absence or mutation indicating predisposition to tumorigenesis upon
CC exposure to mitotic stress). Also claimed is a diagnostic agent, e.g. an
CC antisense fragment of the present sequence, that binds to the Chfr
CC nucleic acid, and a diagnostic kit for detecting tumorigenic potential
CC of a cell. A composition which inhibits the biological activity of Chfr
CC may comprise a ligand selected from an antibody or its fragment. The Chfr
CC inhibitor is used in a claimed method of retarding the growth of a cancer
CC cells. Chfr polypeptides are useful in screening for drugs which can
CC inhibit the activity of Chfr in a cancer cell, rendering the cell more
CC sensitive to additional antitumour therapies

XX Sequence 2679 BP, 650 A; 715 C; 764 G; 550 T; 0 U; 0 Other;

Query Match 100.0%; Score 2679; DB 5; Length 2679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAGAAATTCGGACAGAGCCGCAATGCTTTGACAGCGCGCGCGAGTTCGG 60
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DB 61 GTTCGCGCGCGCGCGCGAGTGTGAATCCGATGAGCGCGCGCGAGAAAGGCAAGAGTCG 120
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DB 121 CGCGCGCGCGAGCCCTGCGGAGCGCTCTGCTGCGCGCGAGAGAGCGCGAGC 180
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XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 994P-00248036.
PR 27-ANG-1999; 993P-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
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PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 12099; 2537bp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dt primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
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XX
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Best Local Similarity 98.6%; Pred. No. 0;
Matches 2633; Conservative 0; Mismatches 1; Indels 36; Gaps 1;
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Db 245 TCTCTGAGATCACTGTAGAAATTGTAGTGAATAATCAGGTGAGGAGCACTGGAAAG 304
Qy 317 ATACGACGACAGTGGAGAGGTGATTAAAGCTGAAGGTTGTTAAGAGCAGACATGCC 376
Db 305 ATACGACGACAGTGGAGAGGTGATTAAAGCTGAAGGTTGTTAAGAGCAGACATGCC 364
Qy 377 CTTTACAGACTGGGAGTGTCACTTGTGTTGTAAGAAATGAACCGGAAACAACAG 436
Db 365 CTTTACAGACTGGGAGTGTCACTTGTGTTGTAAGAAATGAACCGGAAACAACAG 424
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Db 481 -----GATACCTCAGGTGAGGTGAGGCGAG 508
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Db 1409 CCTTGGGGATGACACCTTCCAGTCCGCTGAGCTGACGACAGCTCCAGATTAAGTGT 1468
Qy 1517 GCCCTTGAAGAAAGCCAGCGCTGTGACCTGCTGCTTCAAGCCATGCGCCAGCGGA 1576
Db 1469 GCCCTTGAAGAAAGCCAGCGCTGTGACCTGCTGCTTCAAGCCATGCGCCAGCGGA 1528
Qy 1577 GAGCGAGCGGAGACAGACCCGCGTGTGCGCTCTCAGCAGTGTGCGGTCTGCGTCAAGC 1636
Db 1529 GAGCGAGCGGAGACAGACCCGCGTGTGCGCTCTCAGCAGTGTGCGGTCTGCGTCAAGC 1588
Qy 1637 CTTTCTGACCTGTATCTGGGGCTGACACCGGACCGGCTGTAAAGGCTGCTGGCCCGT 1696
Db 1589 CTTTCTGACCTGTATCTGGGGCTGACACCGGACCGGCTGTAAAGGCTGCTGGCCCGT 1648
Qy 1697 TTTGTGAGCTCAACCTGGGATGACAAGTGTGAGACGGGCTGTAAACAACAAGCTACG 1756
Db 1649 TTTGTGAGCTCAACCTGGGATGACAAGTGTGAGACGGGCTGTAAACAACAAGCTACG 1708
Qy 1757 AGTCAGACATCTGAAGAAATTAAGTGAACAGAGGTTTGAATGAAAAACAATGTTGA 1816
Db 1709 AGTCAGACATCTGAAGAAATTAAGTGAACAGAGGTTTGAATGAAAAACAATGTTGA 1768
Qy 1817 CCGAGAGCTGTGAGGCTTCCAGGGGAGAGTGTCTGCTGTCTGATTAAGAGTCAAGC 1876
Db 1769 CCGAGAGCTGTGAGGCTTCCAGGGGAGAGTGTCTGCTGTCTGATTAAGAGTCAAGC 1828
Qy 1877 GAGACACCGTCTGTGTTAAGTGTGAGGCTGAGGCTGAGGCTGAGCTATCAGT 1936
Db 1829 GAGACACCGTCTGTGTTAAGTGTGAGGCTGAGGCTGAGGCTGAGCTATCAGT 1888
Qy 1937 ATCGGACGAACATTCCTGCTTCCAGGTTGCCAGTGGCCGTTAACATCCGCTGAGCT 1996
Db 1889 ATCGGACGAACATTCCTGCTTCCAGGTTGCCAGTGGCCGTTAACATCCGCTGAGCT 1948
Qy 1997 ACTGGGCGCTGAATGCGCGACCTCAGGTGAAGTCAACCGCATGAATTAATCAATATA 2056
Db 1949 ACTGGGCGCTGAATGCGCGACCTCAGGTGAAGTCAACCGCATGAATTAATCAATATA 2008
Qy 2057 TCTGTGAACAGACAGGTTCAAAAACTAAGCATCAGAGGCTCAGACAGCTTCAAGC 2116
Db 2009 TCTGTGAACAGACAGGTTCAAAAACTAAGCATCAGAGGCTCAGACAGCTTCAAGC 2068
Qy 2117 TGAAGTGAAGAGAGCTGTTTTTAAATACAGACAGACAGCTCAAGGTTTTTACA 2176
Db 2069 TGAAGTGAAGAGAGCTGTTTTTAAATACAGACAGACAGCTCAAGGTTTTTACA 2128
Qy 2177 GCCCCGAGGGAAGGAGACGAGGCTCCGACAGGCTCTGGGGGTGAGCTCTTCTGTG 2236
Db 2129 GCCCCGAGGGAAGGAGACGAGGCTCCGACAGGCTCTGGGGGTGAGCTCTTCTGTG 2188
Qy 2237 AGCTTTTAACTCTGAGTGAAGCCCTCCAGAGCCCGGAGGCGCAGGCGCGCTCC 2296
Db 2189 AGCTTTTAACTCTGAGTGAAGCCCTCCAGAGCCCGGAGGCGCAGGCGCGCTCC 2248

QY	747	TCCTCTGTGGCAAGGATGAAGAGTCTCCAGAGTTTGGCTCAGGCTCCCGACAGAAAGAC	806
Db	558	TCCCTCTGTGGCAAGGATGAAGAGTCTCCAGAGTTTGGCTCAGGCTCCCGACAGAAAGAC	657
QY	807	TGCGTCTTTTGTGTGTTGAAACCCGAGATCAGAGAGATTTTGAGCCCGGTGAGAGAA	866
Db	658	TGCGTCTTTTGTGTGTTGAAACCCGAGATCAGAGAGATTTTGAGCCCGGAGAGAGAA	717
QY	867	AATGAGAGAGATGGGGACCTTGAACCTGAAACGGGACGTTGTGTGTGCACAACCGGTGAG	926
Db	718	AATGAGAGAGATGGGGACCTTGAACCTGAAACGGGACGTTGTGTGTGCACAACCGGTGAG	777
QY	927	AAATCCCCAAAACCGTTCACAGAGAGCTCAGACAGCGGCTGGGAAACCGACAGAGATGGA	986
Db	778	AAATCCCCAAAACCGTTCACAGAGAGCTCAGACAGCGGCTGGGAAACCGACAGAGATGGA	837
QY	987	GGAGACGCTGACATGATCATTCGCCAGGACCTGCTGCACGACTGCTGAGATTTGACAGCC	1044
Db	838	GGAGACGCTGACATGATCATTCGCCAGGACCTGCTGCACGACTGCTGAGATTTGACAGCC	897
QY	1047	CTGACATGCAACGTTCTGCGCGGCTTGTCACTCGGAGCTGGAGAGAGCGCTGCTCCCTGG	1100
Db	898	CTGACATGCAACGTTCTGCGCGGCTTGTCACTCGGAGCTGGAGAGAGCGCTGCTCCCTGG	957
QY	1107	TCCTAATTGCGGCTGTCCCGTGGAGCGGATCTGTAAAAACAATCTTCAACAACCTCGT	1166
Db	958	TCCTAATTGCGGCTGTCCCGTGGAGCGGATCTGTAAAAACAATCTTCAACAACCTCGT	101
QY	1167	GGAAACATATACCTCATTCAGAGATCCAGACAGAGATGGCATGTGAAGAAATGTGCAAAAGAT	1222
Db	1018	GGAAACATATACCTCATTCAGAGATCCAGACAGAGATGGCATGTGAAGAAATGTGCAAAAGAT	1077
QY	1227	GGATGCCAGAATAAATCACTCAAGACATGCTGCAGGCCCAAAGTCAGGCGGTCTTTTTC	1286
Db	1078	GGATGCCAGAATAAATCACTCAAGACATGCTGCAGGCCCAAAGTCAGGCGGTCTTTTTC	1133
QY	1287	TGATGAAGAAGGAGATTCAAGAGAACCTGTGAGAGCTGTGCAGCTTTGACAGTGAATCCTC	1344
Db	1138	TGATGAAGAAGGAGATTCAAGAGAACCTGTGAGAGCTGTGCAGCTTTGACAGTGAATCCTC	1197
QY	1347	AGACATTTAGCAGACATAGTGTGTGTCGCGGACAGTGTCTGTGATCAGAGAGCAGAGCGGC	1400
Db	1198	AGACATTTAGCAGACATAGTGTGTGTCGCGGACAGTGTGTCTGTGATCAGAGAGCAGAGCGGC	1253
QY	1407	GCAAGCTTCCCACTTCCCAAGACACCCGAGAGGCGAGCCAGAGGCCCAAGGCGCTGGGGGA	1466
Db	1258	GCAAGCTTCCCACTTCCCAAGACACCCGAGAGGCGAGCCAGAGGCCCAAGGCGCTGGGGGA	1311
QY	1467	TGCACCCCTTCACGTGTCCGTCAAGTGTGTCGACAGACATTCAGAGATTAACGTGTGCCCTTCA	1522
Db	1318	TGCACCCCTTCACGTGTCCGTCAAGTGTGTCGACAGACATTCAGAGATTAACGTGTGCCCTTCA	1377
QY	1527	AGGAAGCCACGACCCCTGTGTCACTGTGCTTCCAGAGCCCAATGACCCGACCCGAGAGCGGACG	1586
Db	1378	AGGAAGCCACGACCCCTGTGTCACTGTGCTTCCAGAGCCCAATGACCCGACCCGAGAGCGGACG	1433
QY	1587	CGAGCAGGACCCCGGCTGTCCGCCCTCAGACAGTGTCCGATCTGTCTGCAGCCCTTTCTGCGCA	1646
Db	1438	CGAGCAGGACCCCGGCTGTCCGCCCTCAGACAGTGTCCGATCTGTCTGCAGCCCTTTCTGCGCA	1497
QY	1647	CCTGTATCTGGGGGCTGCAACCGGGAACCGGCTGCTACAGGCTGCGGCGCCGTTTGTGACT	1706
Db	1498	CCTGTATCTGGGGGCTGCAACCGGGAACCGGCTGCTACAGGCTGCGGCGCCGTTTGTGACT	1553
QY	1707	CAACCTGGGTGACAAGTGTCTGGAACGAGGCTGTGAACAACAACAGCTTACAGTCAAGCAT	1766
Db	1558	CAACCTGGGTGACAAGTGTCTGGAACGAGGCTGTGAACAACAACAAGCTTACAGTCAAGCAT	1611
QY	1767	CCCTAAGATTAACCTGTGCAACCAAGAGTTTGAATGAAAAACAATGTTGAACCGAGAGCT	1828
Db	1618	CCCTAAGATTAACCTGTGCAACCAAGAGTTTGAATGAAAAACAATGTTGAACCGAGAGCT	1677

[illegible]

Db	241	GGAAAGATGATTTAAACAGCTGAAGTTGTTAAGAGCAGACATGCTCTTTACACATCGG	300
Qy	391	GATGTCATCTACTTGGTGTACAGAGAGATGAACCGAACAACAGTGGCATCTCTAT	450
Db	301	GATGTCATCTACTTGGTGTACAGGAAAGATGAACCGAACAACAGTGGCATCTCTAT	360
Qy	451	GAATCTTTTAAGTAAAGACAGGCGTAGACACAGATCTCTTTGAAGCTTACAGAAAT	510
Db	361	GAATCTTTTAAGTAAAGACAGGCGTAGACACAGATCTCTTTGAAGCTTACAGAAAT	420
Qy	511	GTGTTCCATGAGGACCAAGATACCTCAGGTGCAAGGTGCAAGGCGAGCGGATCCCCG	570
Db	421	GTGTTCCATGAGGACCAAGATACCTCAGGTGCAAGGTGCAAGGCGAGCGGATCCCCG	480
Qy	571	GTCCCTCCGTGTCGCGCCGCACTCAGGTGTGCTTTGAGAAACAAGCCATCAATCG	630
Db	481	GTCCCTCCGTGTCGCGCCGCACTCAGGTGTGCTTTGAGAAACAAGCCATCAATCG	540
Qy	631	ACGTGACACTCTTTCCCAACAGCCTCGCTCTTCCACGAGCCTTCTCTGACGGCGA	690
Db	541	ACGTGACACTCTTTCCCAACAGCCTCGCTCTTCCACGAGCCTTCTCTGACGGCGA	600
Qy	691	GAGCGTTCCTCAGTTGTGGGTCTGGGGGTGTGGCATCTCCCTAAAGAAAGTGTCCC	750
Db	601	GAGCGTTCCTCAGTTGTGGGTCTGGGGGTGTGGCATCTCCCTAAAGAAAGTGTCCC	660
Qy	751	TCTGTGGCAATGATGAGTCTCCAGCTTTCCTCAGCTCTCCGACAGAAAGCTGCG	810
Db	661	TCTGTGGCAATGATGAGTCTCCAGCTTTCCTCAGCTCTCCGACAGAAAGCTGCG	720
Qy	811	TCCTTTTGTGTGTGGAACCCCAAGATCAGAGGATTTGAGCCCTGTAGAGAAATG	870
Db	721	TCCTTTTGTGTGTGGAACCCCAAGATCAGAGGATTTGAGCCCTGTAGAGAAATG	780
Qy	871	AGAAGAGATGGGGAACCTTGAACTTGAACGGGCAAGTTGTGTGTGCAACAACCGCGTAGAAT	930
Db	781	AGAAGAGATGGGGAACCTTGAACTTGAACGGGCAAGTTGTGTGTGCAACAACCGCGTAGAAT	840
Qy	931	GCCCAAAACGTTCACAGAGACGTCAAGACAGCGGCTGGGAAGCCGACAAATGAGAG	990
Db	841	GCCCAAAACGTTCACAGAGACGTCAAGACAGCGGCTGGGAAGCCGACAAATGAGAG	900
Qy	991	ACGTGACATGATCATCTGCGAGGACCTGTGCAACGACTGTAAGTTTGACAGCCCTGC	1050
Db	901	ACGTGACATGATCATCTGCGAGGACCTGTGCAACGACTGTAAGTTTGACAGCCCTGC	960
Qy	1051	ATGCAACAGTTCTGCGGCTTGTCTACTTCGGGCTGGAATGAGCGCTGTCCTGTGTCT	1110
Db	961	ATGCAACAGTTCTGCGGCTTGTCTACTTCGGGCTGGAATGAGCGCTGTCCTGTGTCT	1020
Qy	1111	ACCTGCGCTGCCCCGTGGAGGGATCTGTAAACCAATCTCAACAACCTGTGGAA	1170
Db	1021	ACCTGCGCTGCCCCGTGGAGGGATCTGTAAACCAATCTCAACAACCTGTGGAA	1080
Qy	1171	GCATACCTCATCAGCATCCAGACAAAGAGTGCAGTGAAGAGATGTGCAAGATGAT	1230
Db	1081	GCATACCTCATCAGCATCCAGACAAAGAGTGCAGTGAAGAGATGTGCAAGATGAT	1140
Qy	1231	GCCAGGAATAAATCACTCAAGACATGCTGCAGGCCCAAGTCAGCGGTCCTTTTCTGAT	1290
Db	1141	GCCAGGAATAAATCACTCAAGACATGCTGCAGGCCCAAGTCAGCGGTCCTTTTCTGAT	1200
Qy	1291	GAAGAAAGGAGTTTCAGAGACCTGTGGAGCGTGTCAAGCGTTGACAGTATCCTCAAC	1350
Db	1201	GAAGAAAGGAGTTTCAGAGACCTGTGGAGCGTGTCAAGCGTTGACAGTATCCTCAAC	1260
Qy	1351	ATTAGCAGCCATAGTGTGTGCGGAGAGTGTCTTGAGTACAGAGCAGCGCGCAG	1410
Db	1261	ATTAGCAGCCATAGTGTGTGCGGAGAGTGTCTTGAGTACAGAGCAGCGCGCAG	1320
Qy	1411	CTTCCCACTGCGACACCCGAGGGCAGACCGAGGCCCAAGGCCCTGTGGAGATGCA	1470

Db	1321	CTCTCCCACTGACCGACGACCCGAGGGGAGCGAGAGCAGAGAGCCCCCAACAGAGCCCTTGAGGAGATGCA	1380
Oy	1471	CCCTCCACAGTCCTCGTCAAGCTGTGACGACGACGACGACGTCCAGGATTTACGTGTGCTCCCTCTTCCAAAGGA	1530
Db	1381	CCCTCCACAGTCCTCGTCAAGCTGTGACGACGACGACGACGTCCAGGATTTACGTGTGCTCCCTCTTCCAAAGGA	1440
Oy	1531	AGCCACGCGCTGTGACGACCTGTGCTGTTCGAGCCCAATGCCCGACCGGAGAGCGGAGCGGAG	1590
Db	1441	AGCCACGCGCTGTGACGACCTGTGCTGTTCGAGCCCAATGCCCGACCGGAGAGCGGAGCGGAG	1500
Oy	1591	CAGGACCCGCGCTGTGAGCCCTCCAGCAGATGTGCGGCTGTGCTGACGACCTTTCTGCAACTTG	1650
Db	1501	CAGGACCCGCGCTGTGAGCCCTCCAGCAGATGTGCGGCTGTGCTGACGACCTTTCTGCAACTTG	1560
Oy	1651	TACTGAGGAGCTGACCCGAGACCGGAGCTGTGACGAGCTGTGCTGAGCCGCTTTGTGAGCTCAAC	1710
Db	1561	TACTGAGGAGCTGACCCGAGACCGGAGCTGTGACGAGCTGTGCTGAGCCGCTTTGTGAGCTCAAC	1620
Oy	1711	CTGGGTGACGACGATGTCTGTGACGAGGAGCTGTAAACAACAAGCTACGAGTACGACATCTTG	1770
Db	1621	CTGGGTGACGACGATGTCTGTGACGAGGAGCTGTAAACAACAAGCTACGAGTACGACATCTTG	1680
Oy	1771	AAGAAATTACCTGGCAACCAAGAGTTTGAACATGTGAAAAAACAATGTGACCGGAGGCTCGTG	1830
Db	1681	AAGAAATTACCTGGCAACCAAGAGTTTGAACATGTGAAAAAACAATGTGACCGGAGGCTCGTG	1740
Oy	1831	GCTCTCCACGCGGGAGATGTCTGTCTGTCTGTATTAACAAGTCAAGGAGACACCGTTCTG	1890
Db	1741	GCTCTCCACGCGGGAGATGTCTGTCTGTCTGTATTAACAAGTCAAGGAGACACCGTTCTG	1800
Oy	1891	TGTTACTGCTGTGTGCTGTGCGGACGTTTCCGTGAGCTGACCTTACATGATTCGGCAGAACATT	1950
Db	1801	TGTTACTGCTGTGTGCTGTGCGGACGTTTCCGTGAGCTGACCTTACATGATTCGGCAGAACATT	1860
Oy	1951	CCTGCTTCCGAGTTGCGAGTGGCCGTAACATCCCGTCTGACTCTACTGAGGCGCGTAAC	2010
Db	1861	CCTGCTTCCGAGTTGCGAGTGGCCGTAACATCCCGTCTGACTCTACTGAGGCGCGTAAC	1920
Oy	2011	TGCGGCACTCAGGTGAAGAAGCTCAACACGCGCATGAAATTCATATCTGTGAACAGACA	2070
Db	1921	TGCGGCACTCAGGTGAAGAAGCTCAACACGCGCATGAAATTCATATCTGTGAACAGACA	1980
Oy	2071	AGGTTCAAAAACTTAA 2085	
Db	1981	AGGTTCAAAAACTTAA 1995	
RESULT 6			
ADM03388			
ID	ADM03388	standard; cDNA; 2448 BP.	
XX	AC	ADM03388;	
DT	20-MAY-2004	(first entry)	
DE	Human cDNA of the invention SEQ ID NO:2073.		
XX	ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.		
XX	OS	Homo sapiens.	
XX	PN	EP1347046-A1.	
XX	PD	24-SEP-2003.	
XX	PF	12-APR-2002; 2002EP-00008400.	
XX	PR	22-MAR-2002; 2002JP-00137785.	
XX	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,		
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;		

Pt	Seki N, Ooshikawa T, Otsuka M, Nagahari K, Masuno Y;
Dx	WPI, 2003-723558/69.
Xx	P-PsDB; ADM05831.
Pt	New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
Pt	Claim 1; SEQ ID NO 2073; 305bp; English.
Pt	The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
Cc	Sequence 2448 BP; 618 A; 624 C; 661 G; 545 T; 0 U; 0 Other;
SQ	
XX	Query_Match 71.6%; Score 1919.4; DB 11; Length 2448;
XX	Matches Local_Similarity 88.5%; Pred.No.0;
XX	Matches 2227; Conservative 0; Mismatches 6; Indels 284; Gaps 2
Yy	218 GACGAGTGGCGACTTCCTCCGCCAGCAATAAATGTGCTCTGAGATCACTGTAGA 277
Dd	83 GACCCTGTTGGCAGCTTTCCTCCCGAGAAATAAATGCTCTGTGAATCATCTTAGA 142
Oy	278 TTGTAAGTGAGTAAAAATCATAGTCAAGTGCACCTGAAAGATACCAAGCACAGTGGACA 337
Dd	143 TTGTAAGTGAGTAAAAATCAGGTGAGTGCACCTGAAAGATACCAAGTGGACA 202
Oy	338 TGATTAAACAAGTGAAGTTGTTAAGAACACAAATGCCCTTTAGACAGTGGAGATGCA 397
Dd	203 TGATTAAACAAGTGAAGTTGTTAAGAACACAAATGCCCTTTAGACAGTGGAGATGCA 262
Oy	398 TCCTACTGTGTGACAGAAAGATGAACCGGAAACAACAGTGGCATACCTCTATGAATCTT 457
Dd	263 TCCTACTGTGTGACAGAAAGATGAACCGGAAACAACAGTGGCATACCTCTATGAATCTT 322
Oy	458 TAAAGTAAAAGCAAGGCGATGACACAAGAATCTTTGAAAGTAAACAAGAAAAATGTGCC 517
Dd	323 TAAAGTAAAAGCAAGGCGATGACACAAGAATCTT----- 356
Oy	518 ATGGGACCAAAGATATCTCAGTGTGAGGTGACAGGGCGAGGGCCGATCCCGGGTCCCTC 577
Dd	357 ----- 356
Oy	578 CGTCGCGCCGCGACATCAGGTGTGCTTTGAGAGAACCAAGCATCAATGACGTGAC 637
Dd	357 ----- 356
Oy	638 ACTCTTCCCAACAGCTTCGGCTCTTCCACGAGACTTCTCTGACAGGGCAGAGCGTT 697
Dd	357 ----- 356
Oy	698 CCTCCAGTTGCGGCTCTGGGGGTGGTGGCATTCCTCCCTTAAAGAAAGTGTCTCTGTGG 757
Dd	357 -----TGGGCTCTGGGGGTGGTGGCATTCCTCCCTTAAAGAAAGTGTCTCTGTGG 406
Oy	758 CAAGTATGAAGTCTCCAGACTTTGGCTCAGCTCTGCCAGACAGAAAGACTGGCTCTTTT 817
Dd	407 CAAGTATGAAGTCTCCAGACTTTGGCTCAGCTCTGCCAGACAGAAAGACTGGCTCTTTT 466
Oy	818 CGTCGTTGGAACCCCGAGATCAAGAGATTTTGGAGCCGCTGAAGAAAGAAATGAGAGAG 877
Dd	467 CGTCGTTGGAACCCCGAGATCAAGAGATTTTGGAGCCGCTGAAGAAAGAAATGAGAGAG 526
Oy	878 ATGGGACCTTGAACCTGAACGGGCGACTTTGTTGTCGCAACCGGCTGAATGCCCAA 937

Db	527	ATGGGAACTTGA	CGGACAGTTGTTGGTGCACAA	CCGCTGMAATGCCCAA	586	
Qy	938	CCGTCACAGAGA	CCTCAGACAGCGGCTGGAAAAC	CAGACAGATGAGAGACGCTGA	997	
Db	587	CCGTCACAGAGA	CGTTCAGACAGCGGCTGGAAAAC	CAGACAGATGAGAGACGCTGA	646	
Qy	998	CATGATCATTCG	CCAGAGACCTGCTGCACGAC	CTGGTGAATTTGGACCCCTGCATGCACA	1055	
Db	647	CATGATCATTCG	CCAGAGACCTGCTGCACGAC	CTGGTGAATTTGGACCCCTGCATGCACA	706	
Qy	1058	CGTTCTGCGGAG	CGCTTGGCTACTCGGAGCTGAGAG	CGCTCGCTCTGATCTTACCTGAC	1117	
Db	707	CGTTCTGCGGAG	CGCTTGGCTACTCGGAGCTGAGAG	CGCTCGCTCTGATCTTACCTGAC	766	
Qy	1118	GCTGTCCCGTGA	AGCGGATCTGTAAAAACA	CATCTTCAACAACCTCGTGAAGCATAC	1177	
Db	767	GCTGTCCCGTGA	AGCGGATCTGTAAAAACA	CATCTTCAACAACCTCGTGAAGCATAC	826	
Qy	1178	TCATTCAGACAT	CCAGACAGATGGCAGTGAAGAA	GATGTGMAAGTATGGAATGCCAGGA	1237	
Db	827	TCATTCAGACAT	CCAGACAGATGGCAGTGAAGAA	GATGTGMAAGTATGGAATGCCAGGA	886	
Qy	1238	ATTAATATCATC	CAAGACAATGCTGAGACCCAA	AGCTCAGGCGGCTCTTTCTGATGAAGAG	1297	
Db	887	ATTAATATCATC	CAAGACAATGCTGAGACCCAA	AGCTCAGGCGGCTCTTTCTGATGAAGAG	946	
Qy	1298	GGAGTTCAGAGA	CACTGCTGAGGCTGTACAG	CGTTGACAGTGAAGTCTCAGACATTAGCC	1357	
Db	947	GGAGTTCAGAGA	CACTGCTGAGGCTGTACAG	CGTTGACAGTGAAGTCTCAGACATTAGCC	1008	
Qy	1358	AGCCATACGTG	TGTCGCCGACATGTCTTGATG	ACAGAGCAGCGGCGCAGCCTCCCC	1417	
Db	1007	AGCCATACGTG	TGTCGCCGACATGTCTTGATG	ACAGAGCAGCGGCGCAGCCTCCCC	1068	
Qy	1418	ACTGCCCAAGCA	CCCCGAGGCGAGCAGAGGCCCA	CAGGCCCTGGGGGATGCACCTCTCA	1477	
Db	1067	ACTGCCCAAGCA	CCCCGAGGCGAGCAGAGGCCCA	CAGGCCCTGGGGGATGCACCTCTCA	1128	
Qy	1478	CGTCCGTCAG	CCCTGACAGCAAGCAATGCAGATTA	TGATGTCCTCTGCAAGAAAGCCACG	1537	
Db	1127	CGTCCGTCAG	CCCTGACAGCAAGCAATGCAGATTA	TGATGTCCTCTGCAAGAAAGCCACG	1188	
Qy	1538	CCCTGTGACAC	CTGCTCTTCCAGCCCATGCCGAC	CCGAGAGCGGAGCGCAGACAGACC	1597	
Db	1187	CCCTGTGACAC	CTGCTCTTCCAGCCCATGCCGAC	CCGAGAGCGGAGCGCAGACAGACC	1248	
Qy	1598	CGCGATGTCG	CCCCCAGAGTGGCGGCTGCGAC	CGCTTCTGCCACCTGTGATCTGAGG	1655	
Db	1247	CGCGATGTCG	CCCCCAGAGTGGCGGCTGCGAC	CGCTTCTGCCACCTGTGATCTGAGG	1306	
Qy	1658	GCTGCACCCGGA	CCGCGTGTACAGGCTGCGCGCCG	CTTTTGT-----	1701	
Db	1307	GCTGCACCCGGA	CCGCGTGTACAGGCTGCGCGCCG	CTTTTGT-----	1366	
Qy	1702	-----	-----	-----GAGCTCAA	1709	
Db	1367	GCTTTCCTGCA	GCATCATTTAAAACAGGTAA	CATTGCCCTTCATCTCGCAGAGCTCAA	1428	
Qy	1710	CCGTGGGTGACA	AGTGTCTGGA	CGGCGGTGGA	AAACAACAGCGTACAGATCCT	1789
Db	1427	CCGTGGGTGACA	AGTGTCTGGA	CGGCGGTGGA	AAACAACAGCGTACAGATCCT	1486
Qy	1770	GAAGAATTTAC	CTGCGCAACAGAGGTTTGA	CATGAAAAACA	CATGTTGACCGAGACCTCGT	1829
Db	1487	GAAGAATTTAC	CTGCGCAACAGAGGTTTGA	CATGAAAAACA	CATGTTGACCGAGACCTCGT	1548
Qy	1830	GGCTCTCAGG	CGGAGAGTGTCTGCTGTGATTA	CAGAGTCA	CGGAGACACCGTTC	1889
Db	1547	GGCTCTCAGG	CGGAGAGTGTCTGCTGTGATTA	CAGAGTCA	CGGAGACACCGTTC	1608
Qy	1890	GTTGTTACTG	CTGTGTGGCTGGCAGCTTCC	GTGAGCTGACCTATCAGAT	TGGCAGAAAT	1948


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Db      1425 TACTGCTGGGCTGGGAGCTTCCGTGAGCTGACCTATCAGATGCGAGCAATTCCT 1366
Qy      1954 GCTTCGAGATTGCGAGTGGCCGTAAACATCCCGTCTGACTGCTAGTGGGCGGTAACTGC 2013
Db      1365 GCTTCGAGATTGCGAGTGGCCGTAAACATCCCGTCTGACTGCTAGTGGGCGGTAACTGC 1306
Qy      2014 CGCAGCTCAGGTGAAAGCTCAGCAGCCATGAAATTCATTCATTCGTGAACAGACAG 2073
Db      1305 CGCAGCTCAGGTGAAAGCTCAGCAGCCATGAAATTCATTCATTCGTGAACAGACAG 1246
Qy      2074 TTCAAAAATCAAGATCCAGAGGCGCTGAGAGCTTTCAGAGCTTGAAGAGAGAGG 2133
Db      1245 TTCAAAAATCAAGATCCAGAGGCGCTGAGAGCTTTCAGAGCTTGAAGAGAGAGG 1186
Qy      2134 TGTTTTAAATAACAGAGACAGACAGTGAAGTGTTCACAGGCCCCCTGAGGAGAGG 2193
Db      1185 TGTTTTAAATAACAGAGACAGACAGTGAAGTGTTCACAGGCCCCCTGAGGAGAGG 1126
Qy      2194 AGCGAGGGTCTCCGACAGGTGCTTGGGGTACTCTTCTGTGAGAGCTTTTACCTCTGA 2253
Db      1125 AGCGAGGGTCTCCGACAGGTGCTTGGGGTACTCTTCTGTGAGAG--TTTACCTCTGA 1068
Qy      2254 GTGAGACCTCCCGCAGAGCCCGGGGGCGGAGCCCGCCCTGCTGAGAGCTTGGGAG 2313
Db      1067 GTGAGACCTCCCGCAGAGCCCGGGGGCGGAGCCCGCCCTGCTGAGAGCTTGGGAG 1008
Qy      2314 GGCCTGTGATGAGCAGACAGACAGACAGCAGTCTTCTGTAACATGCGGCGCTCCGC 2373
Db      1007 GGCCTGTGATGAGCAGACAGACAGACAGCAGTCTTCTGTAACATGCGGCGCTCCGC 948
Qy      2374 GAGAGGGGAGTGTGCTCTTTTGTACATTTTCCGAAATTAAGTTAAAGCAAGTCTG 2433
Db      947 GAGAGGGGAGTGTGCTCTTTTGTACATTTTCCGAAATTAAGTTAAAGCAAGTCTG 888
Qy      2434 TTTTCAGAAAAGTTCAAGGAGAAAGGCAAGTTTAAATAAATGTTTCAAGAGAA 2493
Db      887 TTTTCAGAAAAGTTCAAGGAGAAAGGCAAGTTTAAATAAATGTTTCAAGAGAA 828
Qy      2494 GGGAGCATTAAGTTTACAGCTTACAGGACGTACACATATCTCTGCTGGGAAACACA 2553
Db      827 GGGAGCATTAAGTTTACAGCTTACAGGACGTACACATATCTCTGCTGGGAAACACA 768
Qy      2554 GGAATTTATCTATTTTATTTTATAGTGTGGCTTACTCTTCAATTAAGATTAAAT 2613
Db      767 GGAATTTATCTATTTTATTTTATAGTGTGGCTTACTCTTCAATTAAGATTAAAT 708
Qy      2614 GTCACAAACTGAGCAAAATATATATTTTAAATTTTACAAATTGACAAA 2666
Db      707 GTCACAAACTGAGCAAAATATATATTTTAAATTTTACAAATTGACTAAA 655

RESULT 8
AAS25843
ID      AAS25843 standard; cDNA; 1311 BP.
XX
AC      AAS25843;
XX
DT      07-NOV-2001 (first entry)
XX
DE      Human cDNA encoding a novel secreted protein, Seq ID 22.
XX
XX      Human; immunosuppressive; antiarthritic; ssr, antirheumatic; cyostatic;
XX      cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;
XX      antibacterial; virucide; fungicide; ophthalmological; vulnery;
XX      secreted protein; rheumatoid arthritis; hyperproliferative disorder;
XX      cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
XX      cerebral ischemia; angiogenesis; nervous system disorder;
XX      Alzheimer's disease; infection; ocular disorder; corneal infection;
XX      wound healing; epithelial cell proliferation; skin ageing; food additive;
XX      preservative; antiproliferative.
OS      Homo sapiens.

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PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241211P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250310P.
PR 01-DEC-2000; 2000US-0250311P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251579P.
PR 08-DEC-2000; 2000US-0251866P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX
PA
XX

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SW;
XX MPI; 2001-489783/53.
XX P-PSDB; AUI15856.
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 1; SEQ ID NO 22; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed

Query Match 35.3%; Score 945; DB 4; Length 1311;
Best Local Similarity 81.1%; Pred. No. 6.1e-217;
Matches 1267; Conservative 6; Mismatches 7; Indels 282; Gaps 4;

QY 56 TCCGGGTTTCGGCGCGGGGAGATGTGATCCGATGAGCGGCCGAGAAAGCAAC 115
DB 5 TCCGGGTTTCGGCGCGGGGAGATGTGATCCGATGAGCGGCCGAGAAAGCAAC 64
QY 116 AGTCGCGCGCGCGCGGACCTTGGGAGCGGCTCTGTGGCGCGGAGGCGGAGC 175
DB 65 AGTCGCGCGCGCGCGGACCTTGGGAGCGGCTCTGTGGCGCGGAGGCGGAGC 124
QY 176 CGCAGCTCTCTGAGGAAGCGGAGTGGACCATGGGCGGAGAGGTGCGACCTT 235
DB 125 CGCAGCTCTCTGAGGAAGCGGAGTGGACCATGGGCGGAGAGGTGCGACCTT 184
QY 236 CCTTCCCGCAGATTAATGCTCTGAGATCACTGTAATTTAGTGAATAAAT 295
DB 185 CCTTCCCGCAGATTAATGCTCTGAGATCACTGTAATTTAGTGAATAAAT 244
QY 296 CAGGTGAGTGAACCTGGAAGATACCAGACCAAGTGAACAGTGAACAGTGAAG 355
DB 245 CAGGTGAGTGAACCTGGAAGATACCAGACCAAGTGAACAGTGAACAGTGAAG 304
QY 356 TTGTTAAGAGAGCAGATCCCTTTACAGATGGGGATGTCATCTTGGTGAAGGA 415
DB 305 TTGTTAAGAGAGCAGATCCCTTTACAGATGGGGATGTCATCTTGGTGAAGGA 364
QY 416 AGAATGAACCGAACAACAAGTGAATCCTTAAGATCTTTAAGTGAAGGAAGCA 475
DB 365 AGAATGAACCGAACAACA----- 382
QY 476 TGAACAGAAATCCTTGAAGCTAACAGAAAAATGTTCATGGAGCAAAAGATCCT 535
DB 383 ----- 382
QY 536 CAGGTGAGTGAAGGCGAGGCGGATCCCGGGTCCCTCGTGTGCGCGGCAATC 595

DB 383 ----- 382
QY 596 AGGTGTCTTTGAGAACCAAGCCATCAATCGATGAGACTCTTCCCAAGCCT 655
DB 383 ----- 382
QY 656 CGGCTCTTCCAGGAGCCTTCTCTGCAAGGCGAGAGCGCTTCTCAAGTGGGCTG 715
DB 383 ----- -GGTCTG 388
QY 716 GGGGTGTGGCATCTCCCTAAAGAAAGTGTCCCTCTGTGGCAAGTGAATGCTCCA 775
DB 389 GGGGTGTGGCATCTCCCTAAAGAAAGTGTCCCTCTGTGGCAAGTGAATGCTCCA 448
QY 776 GCTTGGCTCAGCTCTCCAGACAGAAAGACTGCGCTCTTTCGTGTGGAACCCAGG 835
DB 449 GCTTGGCTCAGCTCTCCAGACAGAAAGACTGCGCTCTTTCGTGTGGAACCCAGG 508
QY 836 ATCAGAGGATTTGAGAGCCCTGTGAAGAAATGAGAGAGATGGGACCTTGACTGA 895
DB 509 ATCAGAGGATTTGAGAGCCCTGTGAAGAAATGAGAGAGATGGGACCTTGACTGA 568
QY 896 ACGGCGAGTGTGTGTCGACAAACCGGTAAAGATGCCCAACCGTCCAGAGAGCTCA 955
DB 569 ACGGCGAGTGTGTGTCGACAAACCGGTAAAGATGCCCAACCGTCCAGAGAGCTCA 628
QY 956 GAGCAGCGGCTGGAAAGCCAGACAAAGATGAGAGAGAGCGCTGACATGATCTGCCAG 1015
DB 629 GAGCAGCGGCTGGAAAGCCAGACAAAGATGAGAGAGCGCTGACATGATCTGCCAG 688
QY 1016 ACCTCTGACAGACTGCGGTGAATTTTGACCCCTGATGACACGTTTTCGGGGCTTGT 1075
DB 689 ACCTCTGACAGACTGCGGTGAATTTTGACCCCTGATGACACGTTTTCGGGGCTTGT 748
QY 1076 ACTCGGCTGATGAGAGCGCTGCTGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1135
DB 749 ACTCGGCTGATGAGAGCGCTGCTGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 808
QY 1136 TCTGTAAAAACATCTCTCAACAACTCTGTGAAGATGATCTTCAATCCAGATCCAG 1195
DB 809 TCTGTAAAAACATCTCTCAACAACTCTGTGAAGATGATCTTCAATCCAGATCCAG 868
QY 1196 AGAGTCGAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1255
DB 869 AGAGTCGAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 928
QY 1256 TGCTCAGGCGCAAGATCAAGCGGCTCTTTTCTGATGAAGAGGAGATTCAAGAGACTGC 1315
DB 929 TGCTCAGGCGCAAGATCAAGCGGCTCTTTTCTGATGAAGAGGAGATTCAAGAGACTGC 988
QY 1316 TGGAGCTGTGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1375
DB 989 TGGAGCTGTGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1048
QY 1376 GGCAGTGTCTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1435
DB 1049 GGCAGTGTCTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1108
QY 1436 GCGAGCCAGAGAGCCCAAGGCGCTGTGGGAGTGAAGCCTTCAAGTCCGTCAAGCTGA 1495
DB 1109 GCGAGCCAGAGAGCCCAAGGCGCTGTGGGAGTGAAGCCTTCAAGTCCGTCAAGCTGA 1168
QY 1496 CAGCAGTCCAGAGATTAAGTGTGCTCTGTGCAAGAGAGCAGCCTGTGACCTGTGCT 1555
DB 1169 CAGT-----CAGATTAAGTGTGCTCTGTGCAAGAGAGCAGCCTGTGACCTGTGCT 1224
QY 1556 TCCAGCCATGTCGCGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1614
DB 1225 T-CAGCCCATGTCGCGAGCGAGAGTGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1283
QY 1615 CA 1616

DB 1284 CA 1285
RESULT 9
ABX73184
ID ABX73184 standard; DNA; 1311 BP.
XX
AC ABX73184;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human novel polymucleotide #12.
XX
XX Human; gene; ds; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotoxic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN US2002132753-A1.
XX
PD 19-SEP-2002.
XX
PF 17-JAN-2001; 2001US-00764864.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234224P.
PR 25-SEP-2000; 2000US-0234974P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.

Db 1225 T-CAGCCATGCGCCGACCGAGAGTGGAACGCGACAGAGCCCGCGTGCSCCCTTAA 1283
 QY 1615 CA 1616
 Db 1284 CA 1285

RESULT 10
 ADA52592
 ID ADA52592 standard; cDNA; 2186 BP.
 XX
 AC ADA52592;
 XX
 DT 20-NOV-2003 (first entry)
 XX

Human coding sequence, SEQ ID 160.
 DE
 XX

KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW Inflammatory disease; osteoporosis; neurological disease; gene; ss.
 OS Homo sapiens.

PN EPI293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX

PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
 XX
 DR WPI; 2003-395539/38.
 DR P-PSDB; ADA54231.

PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.

PS Claim 1; SEQ ID NO 160; 205bp; English.

CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 2186 BP; 493 A; 555 C; 539 G; 599 T; 0 U; 0 Other;

Query Match 32.7%; Score 876.2; DB 10; Length 2186;
 Best Local Similarity 99.4%; Pred. No. 2.8e-200;
 Matches 890; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1772 AGAATTACCTGGCAACGAGAGTTGACATGAGAAAACATGTTGACGAGAGCTCGTG 1831
 Db 671 AGAATTACCTGGCAACGAGAGTTGACATGAGAAAACATGTTGACGAGAGCTCGTG 730
 QY 1832 CTCCTCAGCGGAGAGTGTCTGTCTGTGATTCAGAGTCAAGGAGACACCGTTCTGT 1891
 Db 731 CTCCTCAGCGGAGAGTGTCTGTCTGTGATTCAGAGTCAAGGAGACACCGTTCTGT 790
 QY 1892 GTTACTGCTGTCGCTGCGGAGCTTCCTGTGAGCTACCTATCAAGTATGCGAACAATTC 1951
 Db 791 GTTACTGCTGTCGCTGCGGAGCTTCCTGTGAGCTACCTATCAAGTATGCGAACAATTC 850

QY 1952 CTGCTTCGAGTTGCGACGTGCGCGTAACTCCGCTCTGACTGTACTGCGGCGGTAACT 2011
 Db 851 CTGCTTCGAGTTGCGACGTGCGCGTAACTCCGCTCTGACTGTACTGCGGCGGTAACT 910
 QY 2012 GCCGCACTCAGTGAAAGCTCAACGAGCTGAAATTAATCAATCTCTGTGAACAGACA 2071
 Db 911 GCCGCACTCAGTGAAAGCTCAACGAGCTGAAATTAATCAATCTCTGTGAACAGACA 970
 QY 2072 GATTCAAAAACCTAAGCATCCAGAGGCGCTGAGCAGCTTTCAGCACTGAGAGTGAAGAG 2131
 Db 971 GATTCAAAAACCTAAGCATCCAGAGGCGCTGAGCAGCTTTCAGCACTGAGAGTGAAGAG 1030
 QY 2132 CGTGTGTTTAAATACAGAGCAAGCAGTCAAGGTGTTTCAAGCCCTGAGGAGAG 2191
 Db 1031 CGTGTGTTTAAATACAGAGCAAGCAGTCAAGGTGTTTCAAGCCCTGAGGAGAG 1090
 QY 2192 GGACGACAGGTCTCCGACAGGTGCTCTGGGGTGAATCTCTCTGTGAGAGCTTTTACCTCT 2251
 Db 1091 GGACGACAGGTCTCCGACAGGTGCTCTGGGGTGAATCTCTCTGTGAGAGCTTTTACCTCT 1148
 QY 2252 GAGTGAGACCTCCCGCAGAGCCCGGGGCGCAGCCCGCTCTGAGAGCGCTGAGG 2311
 Db 1149 GAGTGAGACCTCCCGCAGAGCCCGGGGCGCAGCCCGCTCTGAGAGCGCTGAGG 1208
 QY 2312 AGGCTCTGTGTGATCAGCAGACAGACGAGACGAGCCTTCTGTAAATGCGCGCTCCG 2371
 Db 1209 AGGCTCTGTGTGATCAGCAGACGAGACGAGCCTTCTGTAAATGCGCGCTCCG 1268
 QY 2372 CCGAGAGGGGAGTTTGTCTTTTGTACATTTCCGAACTACAGTTTAAAGCAAGATC 2431
 Db 1269 CCGAGAGGGGAGTTTGTCTTTTGTACATTTCCGAACTACAGTTTAAAGCAAGATC 1338
 QY 2432 TGTGTTTCAAGAAAGTTTCAAGGAGAGGCAAGTTTATCAAAATGTTTCAGAG 2491
 Db 1329 TGTGTTTCAAGAAAGTTTCAAGGAGAGGCAAGTTTATCAAAATGTTTCAGAG 1388
 QY 2492 AAGGAGCATTAAGTTTACAGCTTACAGAGCGTACAAATATCTGCTGCTGGGAAACCA 2551
 Db 1389 AAGGAGCATTAAGTTTACAGCTTACAGAGCGTACAAATATCTGCTGCTGGGAAACCA 1448
 QY 2552 CAGATTTTATCTAATTTTATTTATTAAGGTTGCTATCTCTAATTAAGATTAA 2611
 Db 1449 CAGATTTTATCTAATTTTATTTATTAAGGTTGCTATCTCTAATTAAGATTAA 1508
 QY 2612 ATGTCAAAACTGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2666
 Db 1509 ATGTCAAAACTGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1563

RESULT 11
 AAH06828
 ID AAH06828 standard; cDNA; 816 BP.
 XX
 AC AAH06828;
 XX

DT 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:3663.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EPI074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-00116126.

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX MPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 1: SEQ ID NO 3663; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 CC
 XX Sequence 816 BP; 182 A; 216 C; 253 G; 162 T; 0 U; 3 Other;
 XX
 SQ
 Query Match 27.1%; Score 727; DB 4; Length 816;
 Best Local Similarity 93.5%; Pred. No. 1.5e-164;
 Matches 793; Conservative 0; Mismatches 18; Indels 37; Gaps 2;

QY 437 TGGCATACCTCTATGATATCTTTAAGTAAACCAAGCATGACACAGAATCTTTGAG 496
 DB 425 TGGCATACCTCTATGATATCTTTAAGTAAACCAAGCATGACACAGAATCTTT 480
 QY 497 CTAAACAAGAAAATGTGTTCCATGAGACCAAGATACCTCAGGTGACAGTGAAGGCGAG 556
 DB 481 -----GATACCTCAGGTGACAGTGAAGGCGAG 508
 QY 557 GGGCCGATCCCGGGTCCCTCCGTGTGCGCCGACATCAGGTGTCTTTAGAAACAC 616
 DB 509 GGGCCGATCCCGGGTCCCTCCGTGTGCGCCGACATCAGGTGTCTTTAGAAACAC 568
 QY 617 AGCCATCAACATGACGTGACACTTTCGCCACAGCTCGGCTCTTCCAGGAGCTT 676
 DB 569 AGCCATCAACATGACGTGACACTTTCGCCACAGCTCGGCTCTTCCAGGAGCTT 628
 QY 677 CTCTGACAGGAGGAGAGCGTTCTTCAGTTGTGGGTGTGGGGGTGAGCATCTCCCTTA 736
 DB 629 CTCTGACAGGAGGAGAGCGTTCTTCAGTTGTGGGTGTGGGGGTGAGCATCTCCCTTA 688
 QY 737 AAGGAAGTGTCTCTGTGGCAAGTGAAGTCTCCAGCTTTGCTTCCAGCTTCCAG 796
 DB 689 AAGGAAGTGTCTCTGTGGCAAGTGAAGTCTTCAGCTTTGCTTCCAGCTTCCAG 748
 QY 797 ACAGAAAGCTGCTCTTCTTGTGCGTGAACCCAGAGTACAGAGGA-TTTGAGAGCC 855
 DB 749 ACAGAAAGCTGCTCTTCTTGTGCGTGAACCCAGAGTACAGAGGA-TTTGAGAGCC 808
 QY 856 GTGAAGAA 863
 DB 809 GTGAAGAA 816

RESULT 12
 AAH06846
 ID AAH06846 standard; cDNA; 824 BP.
 AC AAH06846;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DB Human cDNA clone (5'-primer) SEQ ID NO:3681.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX MPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 PS Claim 1: SEQ ID NO 3681; 2537pp + Sequence Listing; English.
 XX

PR	14-AUG-2000	2000US-02252686
PR	14-AUG-2000	2000US-02252706
PR	14-AUG-2000	2000US-02254477
PR	14-AUG-2000	2000US-02257577
PR	14-AUG-2000	2000US-02257587
PR	14-AUG-2000	2000US-02257597
PR	14-AUG-2000	2000US-02262797
PR	14-AUG-2000	2000US-02266817
PR	22-AUG-2000	2000US-02266868
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PR	23-AUG-2000	2000US-02270097
PR	30-AUG-2000	2000US-02286924
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PR	05-SEP-2000	2000US-02295097
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PR	06-SEP-2000	2000US-02304377
PR	06-SEP-2000	2000US-02304387
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PR	08-SEP-2000	2000US-02312447
PR	08-SEP-2000	2000US-02314137
PR	08-SEP-2000	2000US-02314147
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PR	20-OCT-2000	2000US-02417877
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PR 08-NOV-2000; 2000US-0246527P.
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PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
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PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

PA (HUMA-) HUMAN GENOME SCT INC.
PI Rosen CA, Barash SC, Ruben SM,
XX
XX MPI: 2001-468783/53.
DR P-PSDB; LANI6317.
XX
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX
PS Claim 1; SEQ ID NO 483; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage

CC capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present CC sequence encodes a novel secreted protein of the invention. Note: The CC sequence data for this patent did not form part of the printed

Query Match 20.0%; Score 536.6; DB 4; Length 693;

Best Local Similarity 92.5%; Pred. No. 9, 8e-119; Mismatches 608; Conservative 7; Indels 29; Gaps 4;

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QY 1104 GTGTCTACTGCGCGTGTCCGTGAGGAGGATCTGTAAACCACTCTCAACACT 1163
DB 74 GTGTCTACTGCGCGTGTCCGTGAGGAGGATCTGTAAACCACTCTCAACACT 133
QY 1164 CGTGAAGCATACCTTCATCCAGATCCAGACAAAGAGTCCAGTGAAGAATGTGCAAG 1223
DB 134 CGTGAAGCATACCTTCATCCAGATCCAGACAAAGAGTCCAGTGAAGAATGTGCAAG 193
QY 1224 TATGATGCGAGATTAATAATCACTCAGACATGCTGACGCCAAAGTCAAGCGGCTCTT 1283
DB 194 TATGATGCGAGATTAATAATCACTCAGACATGCTGACGCCAAAGTCAAGCGGCTCTT 253
QY 1284 TTCTGATGAGAGGAGGAGTTCAGAGGAGCTGCTGAGAGCTTGAAGCTTGAAGTGAAGTC 1343
DB 254 TTCTGATGAGAGGAGGAGTTCAGAGGAGCTGCTGAGAGCTTGAAGCTTGAAGTGAAGTC 313
QY 1344 CTCAGACATTAAGCCAGCCATATAGCTGTGCTGCGGAGTGTCTGTAGTACAGAAAGCAGGC 1403
DB 314 CTCAGACATTAAGCCAGCCATATAGCTGTGCTGCGGAGTGTCTGTAGTACAGAAAGCAGGC 373
QY 1404 GCGCGACGCTCCCACTGCGCCAGCACCCGAGGGCGAAGCCAGAGCCCAAGGCGCTTGGG 1463
DB 374 GCGCGACGCTCCCACTGCGCCAGCACCCGAGGGCGAAGCCAGAGCCCAAGGCGCTTGGG 433
QY 1464 GSATGACCCCTCCAGCTCCGTCAGAGCTGACAGAGTTCAGATTACGTGTGCGCTCT 1523
DB 434 GSATGACCCCTCCAGCTCCGTCAGAGCTGACAGAGTTCAGATTACGTGTGCGCTCT 489
QY 1524 GCAGAGAAAGCCAGCGCTGTGTGCACTGTCTTCAGGCCATGCCGACCGGAGAGCGGA 1583
DB 490 GCAGAGAAAGCCAGCGCTGTGTGCACTGTCTTCAGGCCATGCCGACCGGAGAGCGGA 548
QY 1584 GGGCAGCAGAGACCCGCGTGTGCGCCCTCAGCAGTGTGGGCTGTGCTGACGCTTTCTG 1643
DB 549 -CGCAGACAGACCCGCGTGTGCGCCCTCAGCAGTGTGGGCTGTGCTGACGCTTTCTG 584
QY 1644 CCACCTGTAAGTGGGCTGACCCGAGACCGGCTGTACAGGCTGCTGCGCCGCTTTTG 1700
DB 585 CCACCTGTAAGTGGGCTGACCCGAGACCGGCTGTACAGTGTGCTGCGCCGCTTTTNG 641

```

RESULT 14

ABX73645 ID ABX73645 standard; DNA; 693 BP.

AC ABX73645;

DT 18-MAR-2003 (first entry)

DE Human novel polynucleotide #473.

KM Human; gene; ds; neural disorder; immune system disorder; renal disorder;

KM muscular disorder; respiratory disease; reproductive disorder;

KM gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;

KM hyperproliferative disorder; inflammatory disease; allergic reaction;

KM blood related disorder; cancer; immunosuppressive; anti-inflammatory;

KM cardiovascular; nephrotropic; cytostatic; anti-allergic; thrombolytic;

KM haemostatic; antiarteriosclerotic.

OS Homo sapiens.

XX US2002132753-A1.

XX 19-SEP-2002.

PF 17-JAN-2001; 2001US-00764864.

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0225267P.

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PR 14-AUG-2000; 2000US-0225270P.

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PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 22-AUG-2000; 2000US-0226868P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 05-SEP-2000; 2000US-0229509P.

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PR 08-SEP-2000; 2000US-0231413P.

PR 21-SEP-2000; 2000US-0234223P.

PR 25-SEP-2000; 2000US-0234427P.

PR 27-SEP-2000; 2000US-0235834P.

PR 29-SEP-2000; 2000US-0236327P.

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PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240606P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.

PR 17-NOV-2000; 2000US-0249299P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251856P.

XX (ROSE/) ROSEN C A.

PA (RUBEN/) RUBEN S M.

PA (BARA/) BARASH S C.

PI Rosen CA, Ruben SM, Barash SC;

XX WPI; 2003-147444/14.

DR P-PSDB; ABUS5385.

XX New polypeptides and nucleic acids, useful in gene therapy for treating,

PT inhibiting or preventing e.g. neural, immune system, muscular,

PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or

PT renal disorders.

PS Claim 1; SEQ ID NO 483; 402pp; English.

XX The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vasculitis), nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukemia), inflammatory reactions and conditions (e.g. psoriasis and
 CC and related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
 CC human novel polynucleotides of the invention

Sequence 693 BP; 145 A; 214 C; 197 G; 123 T; 0 U; 14 Other;

Query Match 20.0%; Score 536.6; DB 8; Length 693;
 Best Local Similarity 92.5%; Pred. No. 9.8e-119;
 Matches 608; Conservative 7; Mismatches 13; Indels 29; Gaps 4;

1044 GGCCTGATGACACAGCTTCTGCGGCTTGTCTACTGCGGCTGATGAGAGCTCTGCTCTT 1103
 14 GGCCTGATGACACAGCTTCTGCGGCTTGTCTACTGCGGCTGATGAGAGCTCTGCTCTT 73
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 74 GTGTCTTACTGCTGCGCTGCTGCTGAGCGGATCTGTAAACCAATCTCTCAACACT 133
 1164 CGTGAAGAGATACCTATCCAGATCCAGACAGAGCTCGGAGAGAGAGAGAGAGAGAGAG 1223
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 1284 TTCTGATGAAGAGAGATTCAGAGAGCTGCTGAGAGCTGTCAAGCTTGAAGAGTGC 1343
 254 TTCTGATGAAGAGAGATTCAGAGAGCTGCTGAGAGCTGTCAAGCTTGAAGAGTGC 313
 1344 CTCAGCATTTAGCCAGCCATACGTCGTGCGGCGGAGTGTCTGATACAGAGAGAGAGC 1403
 314 CTCAGCATTTAGCCAGCCATACGTCGTGCGGCGGAGTGTCTGATACAGAGAGAGAGC 373
 1404 GGGGAGAGCTCCCTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
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 1464 GGATGACACCTTCAGCTCGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
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 1524 GGAG 1583
 490 GGAG 548
 1584 GGGGAG 1643
 549 -CGGAG 584
 1644 CCACTGTAAGTGGGCTGACAG 1700
 585 CCACTGTAAGTGGGCTGACAG 641

RESULT 15
 AAA44336
 ID AAA44336 standard; cDNA; 575 BP.
 XX
 AC AAA44336;

XX 21-AUG-2000 (first entry)
 DT Human secreted expressed sequence tag SEQ ID NO:911.
 XX
 XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; angiogenic; haemostatic;
 KW thrombolytic; antiinflammatory; cyrostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; neuoprotective; neurotropic; antiparkinsonian;
 KW antitumor; osteoprotective; anticonvulsant; antidepressant; antipsoiatric;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
 KW autoimmune disorder; multiple sclerosis; allergic condition;
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW Parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
 KW infection; depression; psoriasis; ss.

OS Homo sapiens.
 XX
 XX WO20021991-A1.
 PN
 XX 20-APR-2000.
 PD
 XX 15-OCT-1999; 99WO-US024206.
 PF
 XX 15-OCT-1998; 98US-0104436P.
 PR
 XX (GENW) GENETICS INST INC.
 PA
 PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Werberg D, Yreacy M, Bowman MR;
 PI WPI; 2000-317938/27.
 DR
 XX
 XX Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (SSTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders.
 PS
 XX Claim 1; Page 437; 803pp; English.

AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (SSTs), isolated from human, mouse, chicken and rat tissue
 CC sources. The SSTs can have a range of activities depending on the
 CC tissues they were isolated from. The activities include: Chemotactic;
 CC proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
 CC haemostatic; thrombolytic; antiinflammatory; cyrostatic; antibacterial;
 CC antifungal; antiviral; antidiabetic; antiaesthetic; vulnerary; antitumor;
 CC osteoprotective; anticonvulsant; and antidepressant. The SSTs can be
 CC used for gene therapy and in vaccines. The SSTs are useful as probes for
 CC the identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the SSTs. Proteins encoded by the SSTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention

Sequence 575 BP; 124 A; 168 C; 165 G; 118 T; 0 U; 0 Other;

Query Match 18.5%; Score 495.8; DB 3; Length 575;
 Best Local Similarity 94.8%; Pred. No. 6e-109;
 Matches 532; Conservative 0; Mismatches 7; Indels 22; Gaps 1;

623 CAACATGACGTCAGACCTCTTCCCAACAGCCTCGGCTCTTCCACGAGAGCTTCTCCTG 682

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Qy      743  GTGGTCCCTCTGTGGCAAGTGAAGTCTCCAGCTTTGGCTCAGCTTCCACAGAA  802
Db      130  GTGGTCCCTCTGTGGCAAGTGAAGTCTCCAGCTTTGGCTCAGCTTCCACAGAA  189
Qy      803  AGACTGCGTCTTTTGTGGTGAAGCCCAAGATCAGAGAGATTGAGCCCGTGAAGA  862
Db      190  AGACTGCGTCTTTTGTGGTGAAGCCCAAGATCAGAGAGATTGAGCCCGTGAAGA  249
Qy      863  AGAAATGAGAGG-----AGATGGGACCTTGACCTGAACGGG  900
Db      250  AGAAATGAGAGAGAAACATCCCTTTCCTGTAGATGGGACCTTGACCTGAACGGG  309
Qy      901  CAGTTGTGTGCGCACACCGCGGTAGAATGCCCAACCGTCCACGAGAGCTCAGAGCA  960
Db      310  CAGTTGTGTGCGCACACCGCGGTAGAATGCCCAACCGTCCACGAGAGCTCAGAGCA  369
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Db      370  GCGGCTGGGAAGCCAGACAAGATGAGAGAGCGCTGACATGCATCTGCGCAGGACCTG  429
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GenCore version 5.1.6
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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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15	714	26.7	938	5	BQ924736
16	708.4	26.4	824	4	BG831289
17	706.2	26.4	940	5	BK409790
18	700	26.1	909	5	BK409791
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GI:6808265
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2297)
Ostenweider, B., Obermaier, B., Deutschenbaur, S., Schaipp, A., Mewes, H.W., Weil, B., Amid, C., Oesanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Submitted (03-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp434N2420) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp434N2420
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

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ORIGIN

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 Matches 1501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 HNC: CAP trapper.
 Mus musculus (house mouse)
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 JOURNAL
 MEDLINE
 PUBMED
 99279253
 10349636
 2
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 20499374
 GENOME
 RESEARCH
 10 (10), 1617-1630 (2000)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes

PUBMED 11042159
 REREFERENCE 3
 AUTHORS Shiba, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Washitani, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN Integrated sequence analysis (RISA) system-384-format
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REREFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REREFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REREFERENCE 6 (bases 1 to 3146)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
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JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL 20499374
MEDLINE 11042159
PUBMED

REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL 20530913
MEDLINE 11076861
PUBMED

REFERENCE
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

TITLE
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

JOURNAL 6 (bases 1 to 2876)
MEDLINE
PUBMED

REFERENCE
6
Aizawa, K., Akiyama, J., Akiyama, T., Akiyama, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akanita, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission

TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

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ORIGIN

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Best Local Similarity 74.7%; Pred. No. 0;
Matches 1862; Conservative 0; Mismatches 583; Indels 46; Gaps 10;

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OY		2307	TGGGCAAGGGCTCGTGGTGGCATGCAGAGCAGA-----GACGAAGCC	2347
Db		2479	AGCCTTCATGTCGGGTGAAGAGATCAGTAGACTGAGATTCTCCCTCCCTCCCATGTGACC	2538
OY		2348	TTTTCTGTAACATGCGGCCGTCGCCGCCGAGAGGGGCAAGTTTGTCTTTTGTACATTTTCC	2407
Db		2539	GCTCTCCCTCGTGTGTGTGTGAGGACAGTGCAGAGTTGTGACTTTTGTATCTTTT--	2596
OY		2408	GAACTACAGTTAAGCAGAGAGTGTGTTTCAGAAAAGTTTCAAGGAGAAAGGCAAGT	2467
Db		2597	----CTACCTTGTAACCTTGACTATGTGTTAAATGGAGAGCTCATGAGAAAAGTTGTGACG	2652
OY		2468	TTATCAAAAAACATTGTTTTCAGSAG--AAGGAGCATTAAGTTTACAGCTCACAGAAC-TA	2524
Db		2653	TGTGTACAGAGCATTTCTCCGGAAGAAAGAAAGAGCATGCTTTTACAGCTCCAGGGGTACA	2712
OY		2525	CACAAATATCTGCTGCTGGGAAAAACACAGCATTTATCTATTTTATTTTAAATAGTT	2584
Db		2713	TAGATATGTCCTCCGTCTGGAAAACACAGCGCTTTGTATAATTTTATTTTAAATAGTT	2772
OY		2585	TGGTGCTATCTTCTTAATTAAGATTAAATGTCACAAACTGAGCACAATATATTAATTT	2644
Db		2773	TGTGCTTATCTTCTTAATTAAGATTAAATTAATTAATAAACTGAGCACAATATCTATTAATTT	2832
OY		2645	ATAATTTCAAATTGACAAAAAATTTTTAAAAA	2675
Db		2833	ATAATTTCAAATTGACTAAAAATTAGGAATA	2863
<hr/>				
RESULT 4				
LOCUS	CR625905			
DEFINITION	CR625905	2412 bp	mRNA	linear
	(human).			
ACCESSION	CR625905			
VERSION	CR625905.1	GI:50506712		
KEYWORDS	HNC; CNSLT_CDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Li, W.B., Grubet, C., Jesse, J. and Polares, D.			
JOURNAL	Full-length cDNA libraries and normalization			
REMARK	Unpublished			
	Contact : Feng Liang Email : fliang@lifetech.com URL :			
	http://fulllength.invitrogen.com/InvitrogenCorporation1600			
	Faraday Avenue			
	2 (bases 1 to 2412)			
REFERENCE	Genoscope.			
AUTHORS	Direct Submission			
TITLE	Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :			
JOURNAL	Bp 191 91006 ENVY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
	- Web : www.genoscope.cns.fr)			
	1st strand cDNA was primed with a NotI-oligo(drf) primer. Five prime			
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
	was normalized. Library was constructed by Life Technologies, a			
	division of Invitrogen.			
FEATURES	Location/Qualifiers			
source	1..2412			
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	/mol_type="mRNA"			
	/db_xref="taxon.9606"			
	/clone="CS0DF017Y119"			
	/tissue_type="Fetal brain"			
	/plasmid="pCMVSPORT 6"			

ORIGIN

Query Match 44.3%; Score 1186.4; DB 3; Length 2412;
 Best Local Similarity 95.4%; Pred. No. 8.4e-296;
 Matches 1257; Conservative 0; Mismatches 51; Indels 10; Gaps 3;

1354 AGCCAGCATACGTCGTGTCGGGAGGTCCTGAGTACAGAGGCGGGGAGCCCT 1413
 530 AGCCAGCATACGTCGTGTCGGGAGGTCCTGAGTACAGAGGCGGGGAGCCCT 589
 1414 CCCCATGTCGACACCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1473
 590 CCCCATGTCGACACCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 649
 1474 TCCAGCTCGCTGAGCTGAGAGAGATTCAGAGATTCAGAGATTCAGAGATTCAG 1533
 650 TCCAGCTCGCTGAGCTGAGAGAGATTCAGAGATTCAGAGATTCAGAGATTCAG 706
 1534 CAGGCGCTGAGCCTGCTGCTTCCAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 1593
 707 CAGGCGCTGAGCCTGCTGCTTCCAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 766
 1594 GAGCGCGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1653
 767 GAGCGCGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826
 1654 TGGGGCTGACCCGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1713
 827 TGGGGCTGACCCGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886
 1714 GGTGACAGATGTCGAGCGGCGGTCGAGCAACAAGAGTACAGAGTACAGAGT 1771
 887 AAAAGAAATATGTTATCTCTGAGTCGAGGAGAGAGTCTTCTGCGACATTTA 946
 1772 ---AGAAATTAAGTGGACACAGAGTGTGACATGAGAAACATGTTGACCGAG 1828
 947 AACAGAAATTAAGTGGACACAGAGTGTGACATGAGAAACATGTTGACCGAG 1006
 1829 TGGCTCTCAGCGGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1888
 1007 TGGCTCTCAGCGGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1066
 1889 TGGTGTACTGCTGTCGCTGTCGCGAGCTTCCGATGAGTACATGATTCGAGAA 1948
 1067 TGGTGTACTGCTGTCGCTGTCGCGAGCTTCCGATGAGTACATGATTCGAGAA 1126
 1949 TTTCTGCTTCCAGAGTTCAGAGTTCGAGTTCAGAGTTCAGAGTTCAGAGT 2008
 1127 TTTCTGCTTCCAGAGTTCAGAGTTCGAGTTCAGAGTTCAGAGTTCAGAGT 1186
 2009 ACTGCGCGACTCAGGTGAGAAAGCTCAGCAGGCGCATGAAATTCATCTGTGA 2068
 1187 ACTGCGCGACTCAGGTGAGAAAGCTCAGCAGGCGCATGAAATTCATCTGTGA 1246
 2069 CAAAGTTCAAAACCTAAGATCCAGAGGCGCTGAGAGCTTCAGAGCTGAGGTAA 2128
 1247 CAAAGTTCAAAACCTAAGATCCAGAGGCGCTGAGAGCTTCAGAGCTGAGGTAA 1306
 2129 GAGCGTGTGTTTAAATTAAGAGAGACAGTCAAGGTGTTTCAAGCGCCCTGAG 2188
 1307 GAGCGTGTGTTTAAATTAAGAGAGACAGTCAAGGTGTTTCAAGCGCCCTGAG 1366
 2189 AAGGAGCGAGGGTCTTCGACAGAGTCTCTGGGGTGAATCTTCTGTGAGCTTT 2248
 1367 AAGGAGCGAGGGTCTTCGACAGAGTCTCTGGGGTGAATCTTCTGTGAGAGC 1424
 2249 TCTGAGTGAAGCCCTCCAGAGGCGCGGGGGGCGAGGCGCGCCCTGAGGTGA 2308
 1425 TCTGAGTGAAGCCCTCCAGAGGCGCGGGGGGCGAGGCGCGCCCTGAGGTGA 1484
 2309 GCGAGGGCTCTGTGTGGCATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2368
 1485 GCGAGGGCTCTGTGTGGCATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1544

QY 2369 CCGCCGAGAGGGGAGGAGTGTGCTGCTTGTGACATTTCCGAAACTACAGTTAAAGCAGA 2428
 DB 1545 CCGCCGAGAGGGGAGGAGTGTGCTTGTGACATTTCCGAAACTACAGTTAAAGCAGA 1604
 QY 2429 GTCTGTTTTCAGGAAAGTTTCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2488
 DB 1605 GTCTGTTTTCAGGAAAGTTTCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1664
 QY 2489 GAGAGGAGCATTAACTTACAGCTTACAGAGAGTACACATATCTGCTGGGAGAA 2548
 DB 1665 GAGAGGAGCATTAACTTACAGCTTACAGAGAGTACACATATCTGCTGGGAGAA 1724
 QY 2549 CCAAGCATTTTATCATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2608
 DB 1725 CCAAGCATTTTATCATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1784
 QY 2609 TAAATGTCAAAACTGTACACAAATTAATTAATTTATTTATTTATTTATTTAT 2666
 DB 1785 TAAATGTCAAAACTGTACACAAATTAATTAATTTATTTATTTATTTATTTAT 1842

RESULT 5
 AL539798 990 bp mRNA linear EST 24-MAR-2004
 LOCUS AL539798 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF031YA23 5-PRIME, mRNA sequence.
 ACCESSION AL539798
 VERSION AL539798.3 GI:45715436
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:31264361.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6792.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DF031YA120P1ec=6792.r.

FEATURES
 source location/Qualifiers
 1..990

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF031YA23"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
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 /note="Torgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 34.2%; Score 917.4; DB 1; Length 990;
 Best Local Similarity 99.2%; Pred. No. 3.6e-226;
 Matches 937; Conservative 5; Mismatches 1; Indels 2; Gaps 2;

61 GTTGGGCGGGGCGGAGTGTGAATCCGATGAGCGGCGGAGAGGAGAGAGAGTGC 120


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Db      20 GTTCCGCGCGGCGGGAATGTAATCCGATGAGCGGCCGAGAGGCAAGCATG 79
Qy      121 CCGCCGCGCGAGCCCTGAGGAGCGGCTCTGCGTGTGGGCGGAGAGGCGAGCGCAC 180
Db      80 CCGCGCGCGGAGCCCTGAGGAGCGGCTCTGCGTGTGGGCGGAGAGGCGAGCGCAC 139
Qy      181 GTCTCTCTTGAAGAGGAGGAGTGAACATCGGGCGGAGACAGAGTTGCGACTTTCTTC 240
Db      140 GTCTCTCTTGAAGAGGAGGAGTGAACATCGGGCGGAGACAGAGTTGCGACTTTCTTC 199
Qy      241 CCAGCAATAAATGCTCTCTGGAAGATCACTGTAATGTAAGTGAATAAATCAGGT 300
Db      200 CCAGCAATAAATGCTCTCTGGAAGATCACTGTAATGTAAGTGAATAAATCAGGT 259
Qy      301 CAGGTGACACTGGAAGATACAGACACAGTGAACAGTGAATTAACAGCTGAAGTTGT 360
Db      260 CAGGTGACACTGGAAGATACAGACACAGTGAACAGTGAATTAACAGCTGAAGTTGT 319
Qy      361 AAGAAGACACATGCGCTTTACAGACTGGGAGTGTCACTACTTGTGTACAGAAAGAT 420
Db      320 AAGAAGACACATGCGCTTTACAGACTGGGAGTGTCACTACTTGTGTACAGAAAGAT 379
Qy      421 GAACCGGAACACAGAGTGGCATCTCTATGATCTTTAAGTGAAGCAAGCATGACA 480
Db      380 GAACCGGAACACAGAGTGGCATCTCTATGATCTTTAAGTGAAGCAAGCATGACA 439
Qy      481 CAGAATCTTTGAAAGCTTACAGAGAAATGTGTTCATGAGGACCAAGATCCTCAGT 540
Db      440 CAGAATCTTTGAAAGCTTACAGAGAAATGTGTTCATGAGGACCAAGATCCTCAGT 499
Qy      541 GCAGGTGACGAGGCGAGGCGGCGATCCCGGGGTCCCTCGGTGTGCGCCGCGCATAGTG 600
Db      500 GCAGGTGACGAGGCGAGGCGGCGATCCCGGGGTCCCTCGGTGTGCGCCGCGCATAGTG 559
Qy      601 TGCTTTGAGGAACAAGCCATCAATGACGTGACAGCTTCTTCCCAAGCCTCGGCC 660
Db      560 TGCTTTGAGGAACAAGCCATCAATGACGTGACAGCTTCTTCCCAAGCCTCGGCC 619
Qy      661 TCTTCCAGGAGACCTTCTCTGAGGAGGAGAGCTTCTCTCAATTTGGGTCTGAGGAGT 720
Db      620 TCTTCCAGGAGACCTTCTCTGAGGAGGAGAGCTTCTCTCAATTTGGGTCTGAGGAGT 679
Qy      721 GGTGACATCTCCCTAAAGAAAGTGTCTCTGTCGCAAGTGAAGTCTCCAGCTTT 780
Db      680 GGTGACATCTCCCTAAAGAAAGTGTCTCTGTCGCAAGTGAAGTCTCCAGCTTT 739
Qy      781 GCTTCACTCTTCCAGAGAAAGACTGCTGCTTTCTGTCGTTGAAACCCGAGGATCAG 840
Db      740 GCTTCACTCTTCCAGAGAAAGACTGCTGCTTTCTGTCGTTGAAACCCGAGGATCAG 799
Qy      841 GAGGATTTGAGGCGCGTGAAGAAATGAGAGAGAGTGGGACCTTGACTTGAACGGG 900
Db      800 GAGGATTTGAGGCGCGTGAAGAAATGAGAGAGAGTGGGACCTTGACTTGAACGGG 858
Qy      901 CAGTTGTTGATGCAACACCGGCTAGAAATGCCCAACCGTCAAGAGAGAGTCAAGACA 960
Db      859 CAGTTGTTGATGCAACACCGGCTAGAAATGCCCAACCGTCAAGAGAGAGTCAAGACA 918
Qy      961 GCGGCTGGGAAGCCAGACAAAGATGAGAGAGAGCTGACATGATC 1005
Db      919 GCGGCTGGGAAGCCAGACAAAGATGAGAGAG-MSCTGACATGATC 962

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RESULT 6
AL539797/c      1118 bp      mRNA      linear      EST 24-MAR-2004
LOCUS      AL539797 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION      CS0DF031YA23 3-PRIME, mRNA sequence.
ACCESSION      AL539797
VERSION      AL539797.3 GI:45715435
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens

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REFERENCE
AUTHORS      Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On Feb 15, 2001 this sequence version replaced gi:31264360.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6792.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0DF031YA12NP1&c=6792.r.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF031YA23"
/tissue_type="FETAL BRAIN"
/dev_stage="Fetal"
/clone_id="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match      34.0%; Score 911.2; DB 1; Length 1118;
Best Local Similarity 91.3%; Pred. No. 1.5e-224;
Matches 973; Conservative 40; Mismatches 47; Indels 6; Gaps 5;

Qy      1580 CGAGCGCGAGCAGAGACCCGCTGCTGCGCCCTCAGAGTGTGCGCTGCTGACGCTT 1639
Db      1060 CGAGCGCGAGCGGCGRSNAAGACCCGCTTCCCTCAGAGKKGCGGTCTGACGCT 1001
Qy      1640 TCTGCACTGTATCTGGGGCTGACACCCGAGACCGGCTGCTGCTGCTGCTGCTTT 1639
Db      1000 TCTGCACTGTATCT-GGGCTGACACCCGAGACCGGCTGCTGCTGCTGCTGCTGCT-TTT 944
Qy      1700 GTGAGCTCAACCTGGTGAACAAGTGTCTGAGCGGCGTGTGAACAACAAGTACAGAGT 1759
Db      943 GKGAGCTCAACCTGGTGAACAAGTGTCTGAGCGGCGTGTGAACAACAAGTACAGAGT 884
Qy      1760 CAGACATCTGAGAAATTAATCTGGCAACAAGGTTTGACATGGAATAAATGTTGACCG 1819
Db      883 CAGACATCTGAGAAATTAATCTGGCAACAAGGTTTGACATGGAATAAATGTTGACCG 824
Qy      1820 AGAGCTCTGGGCTCTCAGCGGAGAGTGTCTGCTGTGATTAAGAGTCAACGGAG 1879
Db      823 AGAGCTCTGGGCTCTCAGCGGAGAGTGTCTGCTGTGATTAAGAGTCAACGGAG 764
Qy      1880 ACAACCTTCTGTATCTAGTGTGCTGCTGCGAGCTTCCGTGAGTCACTATCAGTATC 1939
Db      763 ACAACCTTCTGTATCTAGTGTGCTGCTGCGAGCTTCCGTGAGTCACTATCAGTATC 704
Qy      1940 GGCAGAACATCTCTGCTTCCGAGTTGCGAGTGGCGCTGAATCTCCGCTGACTGCTACT 1999
Db      703 GGCAGAACATCTCTGCTTCCGAGTTGCGAGTGGCGCTGAATCTCCGCTGACTGCTACT 644
Qy      2000 GGGGCGGTAACTGCGGACCTCAGGTGAAGTCAACAAGCGCATGAATTAATATATCT 2059
Db      643 GGGGCGGTAACTGCGGACCTCAGGTGAAGTCAACAAGCGCATGAATTAATATATCT 584
Qy      2060 GTGAACAGACAGATTTCAAAATTAAGATCTCAGAGGCGCTGAGCAGCTTTCAGCACTGG 2119

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Db	583	GTGAACAGACAAGGTTCAAAAACCTAAGCATCCAGAGGCGCCCTGAGACGGTTTCAGACATCG	522
Qy	2120	AGGTGAAGAAGACCGTGTCTTTTAAATACAGAGACAGACACTCAAGGTGTTCACAGCC	2179
Db	523	AGGTGAAGAAGACCGTGTCTTTTAAATACAGAGACAGACACTCAAGGTGTTCACAGCC	464
Qy	2180	CCCTGAGGAAAGGAGACGACGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGC	2239
Db	463	CCCTGAGGAAAGGAGACGACGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGC	404
Qy	2240	TTTTTACCTCTGAGTGAAGACCTTCCCAAGACCCCGGAGGCGCGACGCTCCGCTCTGG	2299
Db	403	---TTTACCTCTGAGTGAAGACCTTCCCAAGACCCCGGAGGCGCGACGCTCCGCTCTGG	346
Qy	2300	TGAGCGCTGGGACGGGCTCTGTGTGGACATCCAGCAGACAGACGAAAGCTTTCTGTGAAT	2358
Db	345	TGAGCGCTGTGSGACAGGCGCCCTGTGTGGACATCCAGCAGACAGACGAAAGCTTTCTGTGAAT	286
Qy	2350	GCGGCGCTCCCGCCGAGAGGGGACGTTTGTCTCTTTGTACATTTTCCGAAACTACAGT	2419
Db	285	GCGGCGCTCCCGCCGAGAGGGGMAATTTTGTCTCTTTGTACATTTTCCGAAACTACAGT	226
Qy	2420	AAAGGAGAAAGTCTGTTTTCAGAAAAGTTTCAAGGGAAGAAGGCAAGTTTATCAAAAACA	2479
Db	225	AAAGGAGAAAGTCTGTTTTCAGAAAAGTTTTCAGGGAAGAAGGCAAGTTTATCAAAAACA	166
Qy	2480	TTGTTTCAGAGAAAGGAGACATTAAGTTTACAGCCTACAGACAGTACAAATATCTGTG	2539
Db	165	TTGTTTCAGAGAAAGGAGACATTAAGTTTTCAGCCTACAGACAGTACAAATATCTGTG	106
Qy	2540	CTGGGAAAACACACAGCATTTTATCTATTTTATTTTAATXAGTTGGTCTTATCTTCT	2599
Db	105	CTGGGAAAACACACAGCGGTTTATSTDTTATTTTAAATXAGTTGGTCTTATCTTCT	46
Qy	2600	AATAAGATTTAAATGTCAAAACTGTACACAAATATATATATTTA	2645
Db	45	AATAAGATTTAAATGTCACTATXGTGTA-YACMAWTAATTAATTTA	1
RESULT 7			
LOCUS	B0876252	876 bp	mRNA linear EST 16-AUG-2002
DEFINITION	AGENCOURT 8681666 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376937		
ACCESSION	B0876252		
VERSION	B0876252.1	GI:22268258	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (Baee 1 to 876)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strusberg, Ph.D. Email: gsr@bbs-riemail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://limage.lnl.nih.gov Plate: L1CM2559 row: 0 column: 18 High quality sequence stop: 678.		
FEATURES			
source			1..876 Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"
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/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

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Query Match	Similarity	Score	DB 5	Length	876	
Best Local	38.3%	Pred. No. 1.7e-201				
Matches	863	Conservative	0	Mismatches	9	Indels
					6	Gaps
						3
QY	1165	GTGAGACATATCCTCATCCAGCATCCAGACAMAGAGTCGACAGTGAAGAAATGTGCCAAAGT	1224			
Db	1	GTGAGAGCATACCTCATCCAGCATCCAGACAMAGAGTCGACAGTGAAGAAATGTGCCAAAGT	60			
QY	1225	ATGATATCCAGGAATATAAATCATCTCAAGACATGCTGCAGGCCCAAAAGTCAGGCGGCTCTTTT	1284			
Db	61	ATGATATCCAGGAATATAAATCATCTCAAGACATGCTGCAGGCCCAAAAGTCAGGCGGCTCTTTT	120			
QY	1285	TCTGATGAAGAAGGAGATTCAGAGAGCACTGCTGGAGCTGCAGAGCTTTGACAGAGAGCC	1344			
Db	121	TCTGATGAAGAAGGAGATTCAGAGAGCACTGCTGGAGCTGCAGAGCTTTGACAGAGAGCC	180			
QY	1345	TCAGACATTTAGCCAGCCATATAGTGTGTGCGGAGAGTGTCCCTGAGTACAGAAAGCAGAGC	1404			
Db	181	TCAGACATTTAGCCAGCCATATAGTGTGTGCGGAGAGTGTCTTAGATACAGAAAGCAGAGC	240			
QY	1405	GCGCAGCCTTCCCATCTGCCCAAGACACCCGAGGGCGAGCCAGAGAGCCCAAGGCCCTTGAGG	1464			
Db	241	GCGCAGCCTTCCCATCTGCCCAAGACACCCGAGGGCGAGCCAGAGAGCCCAAGGCCCTTGAGG	300			
QY	1465	GATGACACCTTCACAGTCCGTTCAGCCCTTACAGACAGTATCCAGATTTACAGTGTGCGCCCTG	1524			
Db	301	GATGACACCTTCACAGTCCGTTCAGCCCTTACAGACAGTATCCAGATTTACAGTGTGCGCCCTG	357			
QY	1525	CAGAGAAAGCAAGCCCTGTGCACATCTGTGCTTCAGGCCATAGCCGACCGAGAGCGAG	1584			
Db	358	CAGAGAAAGCAAGCCCTGTGCACATCTGTGCTTCAGGCCATAGCCGACCGAGAGCGAG	417			
QY	1585	CGCGAGAGGACCCGCGGTGTGCGCCCTCAGACAGTGTGCGGCTGTGCGACGCTTTTCTGC	1644			
Db	418	CGCGAGAGGACCCGCGGTGTGCGCCCTCAGACAGTGTGCGGCTGTGCGACGCTTTTCTGC	477			
QY	1645	CACCTGTATCTGAGGGCTGCACCCGAGACGGGCTGCTACGGCTGTGCGGCCCGGTTTGTGAG	1704			
Db	478	CACCTGTATCTGAGGGCTGCACCCGAGACGGGCTGCTACGGCTGTGCGGCCCGGTTTGTGAG	537			
QY	1705	CTCAACCTGGAGTACAGATGTCTGAGACGGGGTGTGAAACAACAACAGCTTACGAGTCAAGC	1764			
Db	538	CTCAACCTGGAGTACAGATGTCTGAGACGGGGTGTGAAACAACAACAGCTTACGAGTCAAGC	597			
QY	1765	ATCTGGAAGATTACTGTGCAACACCAAGAGTATTGACATGAAAAACATGTTGACCGAGAGC	1824			
Db	598	ATCTGGAAGATTACTGTGCAACCAAGAGTATTGACATGAAAAACATGTTGACCGAGAGC	657			
QY	1825	CTCTGTGCTCTCCAGCGGGAGATGTCTCTGTCTGTATTAACAGATGCAGGG--AGACA	1882			
Db	658	CTCATGTGCTCTCCAGCGGGAGATGTCTCTGTCTGTATTAACAGATGCAGGGAGACAC	717			
QY	1883	CCGTTCTGATTTATCTGTGTGCGGCTGTGAGAGCTTCCGTTAGAGCTATACAGTATCGGC	1942			
Db	718	CCGTTCTGATTTATCTGTGTGCGGCTGTGAGAGCTTCCGTTAGAGCTATACAGTATCGGC	777			
QY	1943	AGAACATTTCTGTCTTCGAGATTGACAGTGTGACAGTAAATCCGTCCTGACCTGCACTGGG	2002			
Db	778	AGAACATTTCTGTCTTCGAGATTGACAGTGTGACAGTAAATCCGTCCTGACCTGCACTGGG	837			
QY	2003	-GCCGTATCTGCCGACCTCAGGTGAAGATTCACACAGC	2039			

Db 838 NCGCGTAACTGCGCACTCCGGTGAAGCTCACCAAGC 875

RESULT 8
LOCUS BUI76559
DEFINITION BUI76559 921 bp mRNA linear EST 04-SEP-2002
AGENCOURT_7940317 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6143609
5', mRNA sequence.
ACCESSION BUI76559
VERSION BUI76559.1 GI:22690543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 921)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13467 row: e column: 18
High quality sequence stop: 697.
Location/Qualifiers
1..921
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6143609"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 28.9%; Score 774.8; DB 5; Length 921;
Best Local Similarity 99.7%; Pred. No. 3.4e-189;
Matches 776; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1889 TGTGTATTGCTGTGTGGCTTGGCCAGCTTCGGTGAAGTCACTATCAAGTATCGGCAGAAC 1948
DB 1 TGTGTATTGCTGTGTGGCTTGGCCAGCTTCGGTGAAGTCACTATCAAGTATCGGCAGAAC 60

QY 1949 TTCTGCTTCCGAGTTGGCAGTGGCCGTAACATCCCGTCTGACGCTAAGTGGGGCGGTA 2008
DB 61 TTCTGCTTCCGAGTTGGCAGTGGCCGTAACATCCCGTCTGACGCTAAGTGGGGCGGTA 120

QY 2009 ACTGCGCACTCAGGTGAAGGCTCAACAGCCCATGAATTCATATCTGTGAACAGA 2068
DB 121 ACTGCGCACTCAGGTGAAGGCTCAACAGCCCATGAATTCATATCTGTGAACAGA 180

QY 2069 CAAGTTCAAAACCTAAGATCAAGAGCCCTTGACAGCTTTGACAGCTGAGGTGAAGA 2128
DB 181 CAAGTTCAAAACCTAAGATCAAGAGCCCTTGACAGCTTTGACAGCTGAGGTGAAGA 240

QY 2129 GAGCGTGTATTAATAACAGAGACAGAGCTCAAGGTTTTCACAGCCCGCTGAAGG 2188
DB 241 GAGCGTGTATTAATAACAGAGACAGAGCTCAAGGTTTTCACAGCCCGCTGAAGG 300

QY 2189 AAGGAGCAGAGGCTCCGACAGAGTGTCTGGGGGTGACTCTTCTGTGTGAGCTTTTACCC 2248
DB 301 AAGGAGCAGAGGCTCCGACAGAGTGTCTGGGGGTGACTCTTCTGTGTGAGCTTTTACCC 360

QY 2249 TCTGATGAGACCTCTCCCAAGAGCCCGGGGGCGCAGACCCGCTCTGTGTAGCGCTG 2308
DB 361 TCTGATGAGACCTCTCCCAAGAGCCCGGGGGCGCAGACCCGCTCTGTGTAGCGCTG 420

QY 2309 GGCAGGGCTCGTGGTGGCATCAGCAGACAGACAGAGCTTTCTGTAACTATGCGGCGCTC 2368
DB 421 GGCAGGGCTCGTGGTGGCATCAGCAGACAGACAGAGCTTTCTGTAACTATGCGGCGCTC 480

QY 2369 CGCGCAGAGGGGCGAGTTTGTCTCTTTGTACATTTTCCGAACTACAGTTAAAGCAGAA 2428
DB 481 CGCGCAGAGGGGCGAGTTTGTCTCTTTGTACATTTTCCGAACTACAGTTAAAGCAGAA 540

QY 2429 GTCTGTTTTCAGAAAGATTTCAGAGGAGAGGCGCAATTATCAAAAACATTGTTTCAG 2488
DB 541 GTCTGTTTTCAGAAAGATTTCAGAGGAGAGGCGCAATTATCAAAAACATTGTTTCAG 600

QY 2489 GAGAAAGGAGCATAGTTTACAGCTTACAGAGCTACAGATATCTCTGCTGGGAAAA 2548
DB 601 GAGAAAGGAGCATAGTTTACAGCTTACAGAGCTACAGATATCTCTGCTGGGAAAA 660

QY 2549 CCACAGCATTTATCTATTTTATTTTATTTATAGGTTTGTGCTTATCTTAAATAGATT 2608
DB 661 CCACAGCATTTATCTATTTTATTTTATTTATAGGTTTGTGCTTATCTTAAATAGATT 720

QY 2609 TAAATGTCACAACTGTAGCACAAAATATATTTATTTATCAAAATGACAAAA 2666
DB 721 TAAATGTCACAACTGTAGCACAAAATATATTTATTTATCAAAATGACAAAA 778

RESULT 9
LOCUS BQ215731 870 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7549119 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059147
5', mRNA sequence.
ACCESSION BQ215731
VERSION BQ215731.1 GI:20397131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 870)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13325 row: f column: 12
High quality sequence stop: 601.
Location/Qualifiers
1..870
/organism="Homo sapiens"
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/clone="IMAGE:6059147"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 68"
/note="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 28.6%; Score 765.4; DB 5; Length 870;

Qy		1091	AACGCTCGCCTGTGATCTTACTGCGCGTGCCGGTAGAGGAACTGTATAAACA	1156
Dp		541	ACGGCTCGTCCTGTGTTCTTACTGCGCGTGTCGCCGAGCGGATCTGTAAAAACCACA	600
Qy		1151	TCTCAACAACCTCGTGAAGCAATCTATCATCAGATTCAGACAAGTGCAGTAAG	1210
Dp		601	TCTCAACAACCTCGTGAAGCAATCTATCATCAGATTCAGACAAGTGCAGTAAG	660
Qy		1211	AAGATGTGCAAGTATGATGTCAGGAATAAATACATCAAG-ACATGTGAGGCCAAA	1265
Dp		661	AAGATGTGCAAGTATGATGTCAGGAATAAATACATCAAGATGCTGAGGCCAAA	720
Qy		1270	GTCAGCGCGTCTTTTTCTGATGAAGAAGGAGTTCAAGAACCTGCT-GGAGCTGTGAG-	1327
Dp		721	GTCAGCGCGTCTTTTTCTGATGAAGAAGGAGTTCAAGAACCTGCTGAGAACCTGTGAGA	780
Qy		1328	ACGTTGACAGTGAG-TCTCAACAACATTAGCCAGCACATAGTGTGTGCCGGAGATGTCT	1386
Dp		781	ACGTTGACAGTGAGTCTCAACAACATTAGCCAGCCCCCTTACTTGTGGGCGCGGAGT	840
Qy		1387	GAGTAC 1392	
Dp		841	GGGTCC 846	
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LOCUS	CD243458	877 bp	mRNA	linear EST 22-MAY-2003
DEFINITION	AGENCOURT_14121909 NIH MGC_180 Homo sapiens cDNA clone IMAGE:30383176 5', mRNA sequence.			
ACCESSION	CD243458			
VERSION	CD243458.1	GI:31003922		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 877)			
JOURNAL	Nih-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rgs@nih-mail.nih.gov Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: NDAM446 row: j column: 17 High quality sequence stop: 660. Location/Qualifiers 1..877 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30383176" /lab_host="DH10B-Ton A (T1 and T5 phage resistances)" /clone_id="NIH_MGC_180" /note="Organ: Testis; Vector: pCMV-SPORT6.1, Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC library."			
FEATURES	source			
ORIGIN				
Query Match	28.3%;	Score 757.6;	DB 6;	Length 877;
Best Local Similarity	96.9%;	Pred. No. 9,66-185;		
Matches 772;	Conservative 0;	Mismatches 25;	Indels 0;	Gaps 0;
1527	AGGAAGCAGCCCTGTGACCTGTGCTTCACGCCCATGCGCCGACGGAGAGCGAGCG	1586		

Db	4	AGGAAGCCACGCCCTGTGTGACCTGTGCTTTCAGGCCATGCCCAGACCGAGACCGAGCG	63
QY	1587	CGAGCAGGACCCGCGGTGTGCGCCCTCAGCAGGTGCGGTCTGCTCGACGCTTTTCTGCCA	1646
Db	64	CGAGCAGGACCCGCGGTGTGCGCCCTCAGCAGGTGCGGTCTGCTCGACGCTTTTCTGCCA	123
QY	1647	CCTGTACTGCGGGCTGCAACCGGACCGGGTGTCTAGCGGCTGCGCCGCTTTTGTGACT	1706
Db	124	CCTGTACTGCGGGCTGCAACCGGACCGGGTGTCTAGCGGCTGCGCCGCTTTTGTGACT	183
QY	1707	CAACCTGGGTGACAAGTGTCTG3ACG3GCTGTGAAACAACAAGCTACGAGTACAGAT	1766
Db	184	CAACCTGGGTGACAAGTGTCTG3ACG3GCTGTGAAACAACAAGCTACGAGTACAGAT	243
QY	1767	CCTGAAGAATTACTGCGCAACCGAGGTTTGCATGAAAAATGTTGACCGAGAGCTT	1822
Db	244	CCTGAAGAATTACTGCGCAACCGAGGTTTGCATGAAAAATGTTGACCGAGAGCTT	303
QY	1827	CGTGGCTCTCCAGCGGGAGGTGTTCTGCTGTGATTAACAAGTCAAGGAGACACCGT	1886
Db	304	CGTGGCTCTCCAGCGGGAGGTGTTCTGCTGTGATTAACAAGTCAAGGAGACACCGT	363
QY	1887	TCGTGTACTCTGTGTGCGCTGTGCGAGCTTCCGTGAGCTGACCTATCGACAGAA	1946
Db	364	TCGTGTACTCTGTGTGCGCTGTGCGAGCTTCCGTGAGCTGACCTATCGACAGAA	423
QY	1947	CATTCCGCTTCCGAGTTGGACAGTGGCGCGTAAACATCCCGTCTGACCTGCTGCGGCGG	2006
Db	424	CATTCCGCTTCCGAGTTGGACAGTGGCGCGTAAACATCCCGTCTGACCTGCTGCGGCGG	483
QY	2007	TAACTGCGCAGCTCAGGTGAAGGCTCAACAAGCCATGAATAATTCATCATCTGTGAACA	2066
Db	484	TAACTGCGCAGCTCAGGTGAAGGCTCAACAAGCCATGAATAATTCATCATCTGTGAACA	543
QY	2067	GACAAAGTTCAAAAACCTAAGATTCACAGAGGCCCTGAGCAGCTTTCAGCATCTGAGGTAA	2126
Db	544	GACAAAGTTCAAAAACCTAAGATTCACAGAGGCCCTGAGCAGCTTTCAGCATCTGAGGTAA	603
QY	2127	GAGAGCGTGTTTTAAATAACAGAGACAAGACGTCAAAGTGTGTTTCAACAGCCCTCTAG	2186
Db	604	GAGAGCGTGTTTTAAATAACAGAGACAAGACGTCAAAGTGTGTTTCAACAGCCCTCTAG	663
QY	2187	GGAAGGGAACGAGGCTCTCCGACAGGTGCTCTGCGGTGACTCTTCTGTGAGCTTTTAC	2246
Db	664	GGAAGGGAACGAGGCTCTCCGACAGGTGCTCTGCGGTGACTCTTCTGTGAGCTTTTAC	723
QY	2247	CCTCTGAGTGAAGACCTCCCGAGAGCCCGGGGGCGCGAGCGGCGCTCCGTGTGAGGC	2306
Db	724	CCTCTGAGTGAAGACCTCCCGAGAGCCCGGGGGCGCGAGCGGCGCTCCGTGTGAGGC	783
QY	2307	TGGGCAAGGCGCTCGTGT 2323	
Db	784	GCGCTGTGGGCAAGGCT 800	

RESULT 12

BU148471

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BU148471 910 bp mRNA linear EST 03-SEP-2002

AGNCOURT 8675647 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6380102

5', mRNA sequence.

BU148471

BU148471.1 GI:22662003

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 910)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: c9apbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM2568 row: c column: 15
 High quality sequence stop: 620.

FEATURES

source

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 /clone="IMAGE:6380102"
 /issue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 40"
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

ORIGIN

Query Match

Best Local Similarity 91.1%; Pred. No. 2.5e-180;
 Matches 858; Conservative 0; Mismatches 40; Indels 44; Gaps 5;

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QY 12 AGGAGGCGCATGTCTTTGACAGCGCGCGCGCGCGCGGTTCCGGGTTGCGCGCG 71
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QY 72 GCGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 131
DB 65 GCGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 124
QY 132 GCGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 191
DB 125 GCGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 184
QY 192 GAAAGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 251
DB 185 GAAAGCGGAGTGTGATCCCGATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
QY 252 ACTGGCTCTGAGATCACTGATGATTTGATGATGATGATGATGATGATGATGATG 311
DB 245 ACTGGCTCTGAGATCACTGATGATTTGATGATGATGATGATGATGATGATGATG 304
QY 312 GGAAGATACAGACCAAGTGAACAGTGAATTAAGTGAATTAAGTGAATTAAGTGA 371
DB 305 GGAAGATACAGACCAAGTGAACAGTGAATTAAGTGAATTAAGTGAATTAAGTGA 364
QY 372 ATGCCCTTTACAGACTGGGAGTGTCTTACTTGTGTGATCAAGAGATGAACCGGAA 431
DB 365 ATGCCCTTTACAGACTGGGAGTGTCTTACTTGTGTGATCAAGAGATGAACCGGAA 424
QY 432 CAACGCGGATACCTCTATGATCTTTAAGTGAACCAAGGATGACCAAGAAATCTT 491
DB 425 CAACGCGGATACCTCTATGATCTTTAAGTGAACCAAGGATGACCAAGAAATCTT 484
QY 492 TGAAGCTTAAAGAAATGTGTTCCATGGGACCAAGATATCCTCAGTGCAGTGCAG 551
DB 485 T-----GATACCTCAGGTGCGAGGTGCAAG 508
QY 552 GCGAGGCGCGCATCCCGGCTCCCTCGTGTGCGCGCGCGCATCAGGTGTGCTTTGAG 611
DB 509 GCGAGGCGCGCATCCCGGCTCCCTCGTGTGCGCGCGCGCATCAGGTGTGCTTTGAG 568

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QY 612 ACCACAGCATCAATCATGACGTCAGACCTCTTCCCAAGCGCTCGGCTCTTCAAGCA 671
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QY 672 GCTTCTCTGCAAGGCGGAGAGGTTCTTCAAGTGTGAGTGTGAGGAGTGTGAGTGT 731
DB 629 GCTTCTCTGCAAGGCGGAGAGGTTCTTCAAGTGTGAGTGTGAGGAGTGTGAGTGT 688
QY 732 CCTTAAGGAAGTGTCTCTGTGCAAGTGAATGATGATGATGATGATGATGATGATG 791
DB 689 CCTTAAGGAAGTGTCTCTGTGCAAGTGAATGATGATGATGATGATGATGATGATG 748
QY 792 CCACAGCAAGAAAGACT-GGTCCTTTTCTGCTGTGGAACCCAGATCAGAGAGATTGG 850
DB 749 CCACAGCAAGAAAGACTGGGCTCTTTTCTGCTGTGGAACCCAGATCAGAGAGATTGG 808
QY 851 AGCCCTGTGAAGAAATGA---GAGGAGATGGGAGCTTG-ACCTGAACGGGCACT 904
DB 809 GAGAGCCGTGAAGAAATGA---GAGGAGATGGGAGCTTG-ACCTGAACGGGCACT 868
QY 905 TGTGTGTCGACCAACC-GGCTAGAAATGCCCAACCGTCCAC 945
DB 869 GTGTGTTCACCAACCAGGAGTGAATGCCCAACCGGCTCC 910

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RESULT 13

BG395714

LOCUS

DEFINITION

602458365F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4580633 5',
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: LNCM1300 row: a column: 18
 High quality sequence stop: 775.

FEATURES

source

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 /db_xref="taxon:9606"
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 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

ORIGIN

Query Match

Best Local Similarity 95.8%; Pred. No. 6.4e-177;
 Matches 779; Conservative 0; Mismatches 31; Indels 3; Gaps 3;

QY 1294 GAAGGAGTTGAGAGGAGCTGCTGAGCTGTGACAGCTTGAAGTGTCTTCAAGATT 1353
 DB 2 GAAGGAGTTGAGAGGAGCTGCTGAGCTGTGACAGCTTGAAGTGTCTTCAAGATT 61
 QY 1354 AGCCAGCCTAGAGTGTGTGCGGGGAGTGTCTTGAAGTGTGAAGAGGCGGCGAGCTT 1413
 DB 62 AGCCAGCCTAGAGTGTGTGCGGGGAGTGTCTTGAAGTGTGAAGAGGCGGCGAGCTT 121
 QY 1414 CCCCACTGCCAGACCCGAGGGCGAGGAGAGGCCCAAGGCCCTGGGGGATGACCC 1473
 DB 122 CCCCACTGCCAGACCCGAGGGCGAGGAGAGGCCCAAGGCCCTGGGGGATGACCC 181
 QY 1474 TCCAGCTCCGTGAGCTGAGACAGACAGTTCAGAGATTAGTGTGCTTGAAGAGC 1533
 DB 182 TCCAGCTCCGTGAGCTGAGACAGACAGTTCAGAGATTAGTGTGCTTGAAGAGC 241
 QY 1534 CAGCCCTGTGACCTGCTGCTTCCAGCCATGCCCCGAGCGGAGAGCGGAGCGAGCAG 1593
 DB 242 CAGCCCTGTGACCTGCTGCTTCCAGCCATGCCCCGAGCGGAGAGCGGAGCGAGCAG 301
 QY 1594 GACCCGCTGTGCGCCCTCAGACAGTGTGCGGTCTGCTGACAGCTTTCGACCTGTAC 1653
 DB 302 GACCCGCTGTGCGCCCTCAGACAGTGTGCGGTCTGCTGACAGCTTTCGACCTGTAC 361
 QY 1654 TGGGGGCTGACCCGAGCGGGCTGACAGCGGCTGCGCCGCTTTTGTGAGTCAACTG 1713
 DB 362 TGGGGGCTGACCCGAGCGGGCTGACAGCGGCTGCGCCGCTTTTGTGAGTCAACTG 421
 QY 1714 GGTGACAAAGTGTGTGACCGCGCTGTGTAACAACAAGCTACAGATCAGACATCTGAAG 1773
 DB 422 GGTGACAAAGTGTGTGACCGCGCTGTGTAACAACAAGCTACAGATCAGACATCTGAAG 481
 QY 1774 AATTACTGTGCAACCAAGAGTTTGAACATGTAAGAAATGTTGACCGAGAGCTGTGCT 1833
 DB 482 AATTACTGTGCAACCAAGAGTTTGAACATGTAAGAAATGTTGACCGAGAGCTGTGCT 541
 QY 1834 CTCGACGGGGAGTGTCTGCTGTGTAACAAGTACAGGAGACACCGCTTGTGT 1893
 DB 542 CTCGACGGGGAGTGTCTGCTGTGTAACAAGTACAGGAGACACCGCTTGTGT 601
 QY 1894 TACTGCTGTGCTGCGAGCTTCCGTGAGCTGACCTATCAGTATCGGACAGAACTTCT 1953
 DB 602 TACTGCTGTGCTGCGAGCTTCCGTGAGCTGACCTATCAGTATCGGACAGAACTTCT 661
 QY 1954 GCTTCCGAGTGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013
 DB 662 GCTTCCGAGTGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
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 DB 722 GCACTCAAGGTGAAGTCAACCAAGCATGAATTAATCATATCTGTGAGACAGAGAC 781
 QY 2071 AGTTCAAAATAAGATCCAGAGCGCTTGAAG 2103
 DB 782 AGTTCAAAATAAGATCCAGAGCGCTTGAAG 814
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 LOCUS AGENCOURT 8779684 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:5371968
 DEFINITION 5', mRNA sequence.
 ACCESSION B036072
 VERSION B036072.1 GI:22351455
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 953)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
<http://image.llnl.gov>
 Plate: ILNLI2546 row: P column: 17
 High quality sequence stop: 630.
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5371968"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN
 Query Match 27.1%; Score 726.8; DB 5; Length 953;
 Best Local Similarity 93.0%; Pred. No. 9.5e-177;
 Matches 842; Conservative 0; Mismatches 18; Indels 45; Gaps 6;
 QY 45 GCGAGCGCGTTCGCGGTTGCGGCGGGGCGGAGTGTGATCCCGATGAGCGGCGCGA 104
 DB 1 GCGAGCGCGTTCGCGGTTGCGGCGGGGCGGAGTGTGATCCCGATGAGCGGCGCGA 60
 QY 105 GAAAGCAAGCAGTGCAGCGCGCGCGAGCCCTGAGGAGCGGCTCTGCGTGTGCGCGGA 164
 DB 61 GAAAGCAAGCAGTGCAGCGCGCGCGAGCCCTGAGGAGCGGCTCTGCGTGTGCGCGGA 120
 QY 165 GGAAGGAGAGCGCGAGCTCTCTGAGAGAGCGGAGTGTGACCATCGGCGGAGACAGAG 224
 DB 121 GGAAGGAGAGCGCGAGCTCTCTGAGAGAGCGGAGTGTGACCATCGGCGGAGACAGAG 180
 QY 225 TTGCGACCTTCTCTCCCGCAATAAAGTGTCTGAGATCACTGTGAATTGTAGT 284
 DB 181 TTGCGACCTTCTCTCCCGCAATAAAGTGTCTGAGATCACTGTGAATTGTAGT 240
 QY 285 GGAATGAATAATCAGTGTGAGTGTGACATGGAAGATCCAGACCAAGTGAATTA 344
 DB 241 GGAATGAATAATCAGTGTGAGTGTGACATGGAAGATCCAGACCAAGTGAATTA 300
 QY 345 CAAGCTGAAGTGTGAAGAGAGAGATGCCCTTTAACAAGGAGATGTCACTT 404
 DB 301 CAAGCTGAAGTGTGAAGAGAGAGATGCCCTTTAACAAGGAGATGTCACTT 360
 QY 405 GGTGTACAGAGAGATGAACCGAGACCAAGTGTGATCCTCATGAATCTTTAAGTGA 464
 DB 361 GGTGTACAGAGAGATGAACCGAGACCAAGTGTGATCCTCATGAATCTTTAAGTGA 420
 QY 465 AAAGCAAGCATGACACAAATCTTTGAAGCTAACAGAGAAATGTTCATGAGAC 524
 DB 421 AAAGCAAGCATGACACAAATCTTT----- 448
 QY 525 CAAAGATACCTCAGGTGACAGTGCAGGAGGAGGCGGATCCCGGCTCCCTCGGTGC 584
 DB 449 ----GATACCTCAGGTGACAGTGCAGGAGGAGGCGGATCCCGGCTCCCTCGGTGC 504
 QY 585 GCCCGCACTCAGGTGTCTTTGAGAGAACCAAGCATCAATCAAGTCAAGCTCTT 644

Db 505 GCCCGCACTCAGTGTGCTTTGAGAACACAGCCATCATGACGTGACAGCTTT 564
 Qy 645 CCCCAACAGCTGGGCTCTTTCCACGAGAGCTTCTCTGACGGGCGAGAGCTTCTCCAG 704
 Db 555 CCCCAACAGCTGGGCTCTTTCCACGAGAGCTTCTCTGACGGGCGAGAGCTTCTCCAG 624
 Qy 705 TTGTGGGTCT-GGGGGTGGTGGGATCTCCCTTAAAGAGTGGTCCCTCTGTGGCAAGT 763
 Db 625 TTGTGGGTCTGGGGGTGGTGGGATCTCCCTTAAAGAGTGGTCCCTCTGTGGCAAGT 684
 Qy 764 ATGAAGTCTCAGCTTGTGCTTCTCTCCACAGAGAAAGATCTGCTCC-TTTTGTGTG 822
 Db 685 ATGAAGTCTCAGCTTGTGCTTCTCTCCACAGAGAAAGATCTGCTCCCTTTTGTGTG 744
 Qy 823 TTGGAACCCCAAGATC-AGAGGATTTGAGAGCCCTGAAAGAAATGAGAGAGATG 880
 Db 745 TTGGAACCCCAAGATCAGAGAGATTTGAGAGCCCTGAAAGAAATGAGAGAGATG 804
 Qy 881 GGGACCTT--GACCTGAACGGGAGTGTGTG--TGACACACGGCGTGAAGATGCCCA 935
 Db 805 GGGACCTTGTGACCTGAGCGGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 864
 Qy 936 AACCG 940
 Db 865 AACCG 869

RESULT 15
 BQ924736 938 bp mRNA linear EST 20-AUG-2002
 LOCUS BQ924736
 DEFINITION AGENCOURT 8853777 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374110
 5' mRNA sequence.

ACCESSION BQ924736
 VERSION BQ924736.1 GI:22339767
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2552 row: 1 column: 23
 High quality sequence step: 629.

FEATURES
 source location/Qualifiers
 1..938

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6374110"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGGCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 26.7%; Score 714; DB 5; Length 938;
 Best Local Similarity 89.7%; Pred. No. 28-173;
 Matches 874; Conservative 0; Mismatches 47; Indels 53; Gaps 8;

Qy 48 CAGCGGTTCCGGGTTCCGGGCGGGGCGGGGATGTAATCCGATGAGCGGCCGAGGA 107
 Db 1 CAGCGGTTCCGGGTTCCGGGCGGGGCGGGGATGTAATCCGATGAGCGGCCGAGGA 60
 Qy 108 AGGCAACAGTGGCGCGCGCCGAGCCTTGGGGAAGGCTCTGTGGTCTGGGCGCGGAGA 167
 Db 61 AGGCAACAGTGGCGCGCGCCGAGCCTTGGGGAAGGCTCTGTGGGCGCGGAGA 120
 Qy 168 GGGCGAGCGGCGAGTCTCTGAGGAAGGGAGTGAACATCGGGCGGAGAAGAGTTG 227
 Db 121 GGGCGAGCGGCGAGTCTCTGAGGAAGGGAGTGAACATCGGGCGGAGAAGAGTTG 180
 Qy 228 CGACCTTCTCTCCCGAGCAATAACTGTCTCTGAGATCACTGATTAATGATGGA 287
 Db 181 CGACCTTCTCTCCCGAGCAATAACTGTCTCTGAGATCACTGATTAATGATGGA 240
 Qy 288 TGAATAATCAGTCAAGTGAACCTGGAAGATCCAGCACAGTGAACAGTATTACAA 347
 Db 241 TGAATAATCAGTCAAGTGAACCTGGAAGATCCAGCACAGTGAACAGTATTACAA 300
 Qy 348 GCTGAAGGTTGTTAAGAGCAGACATGCCCTTACAGACTGGGGATGATCTACTGTGT 407
 Db 301 GCTGAAGGTTGTTAAGAGCAGACATGCCCTTACAGACTGGGGATGATCTACTGTGT 360
 Qy 408 GTACAGGAAGATGAACCGGAACACACAGTGCATCACTTATGATCTTTAAGTGAANA 467
 Db 361 GTACAGGAAGATGAACCGGAACACACAGTGCATCACTTATGATCTTTAAGTGAANA 420
 Qy 468 GCAAGGCATGACACAAGAACTCTTGAAGCTAAACAAGAAATGTGTTCCATGGACCA 527
 Db 421 GCAAGGCATGACACAAGAACTCTT----- 445
 Qy 528 AGATACCTCAGGTGAGGTGAGGGGAGGGGCGGATCCCGGGTCCCTCGTGGCGCC 587
 Db 446 AGATACCTCAGGTGAGGTGAGGGGAGGGGCGGATCCCGGGTCCCTCGTGGCGCC 504
 Qy 588 CCCCACTCAGTGTGCTTTGAGAAACACAGGCATCAACATGAGCTGAGACTCTTCCC 647
 Db 505 CCCCACTCAGTGTGCTTTGAGAAACACAGGCATCAACATGAGCTGAGACTCTTCCC 564
 Qy 648 CACAGCTTGGCTCTTCCACGAGCTTCTCTGAGGGGCGAGAGCTTCTTCAAGTTG 707
 Db 565 CACAGCTTGGCTCTTCCACGAGCTTCTCTGAGGGGCGAGAGCTTCTTCAAGTTG 624
 Qy 708 TGGGTCTGGGGGTGGTGGGATCTCCCTTAAAGGAGTGTCTCTGTGGGCAAGTATG 766
 Db 625 TGGGTCTGGGGGTGGTGGGATCTCCCTTAAAGGAGTGTCTCTGTGGGCAAGTATG 684
 Qy 767 AAGTCTCAGCTTGTGCTTCCAGAGAGAGCTGCTCTTTTGTGCTGTGG 826
 Db 685 AAGTCTCAGCTTGTGCTTCCAGAGAGAGCTGCTCTTTTGTGCTGTGG 744
 Qy 827 AA-CCCAAGATCAGAGAGATTTGAAGCC-----GTGAAGAAATGAGAGATG 880
 Db 745 AA-CCCAAGATCAGAGAGATTTGAAGCC-----GTGAAGAAATGAGAGATG 804
 Qy 881 GGGACCTTGAAGCTGAA-----CGGCAAGTGTGTGCGCAACCGCGTGAAGATGCCCA 935
 Db 805 GGGACCTTGAAGCTGAA-----CGGCAAGTGTGTGCGCAACCGCGTGAAGATGCCCA 864
 Qy 936 AACCTTCAAG 990
 Db 865 AACCTTCAAG 924
 Qy 991 ACGCTGACATGAT 1004
 Db 925 ACGCTGACATGAT 938

Sun Jan 16 16:00:06 2005

us-10-048-046-1.rst

Page 16

Search completed: January 15, 2005, 06:17:46
Job time : 8064 secs

Best Local Similarity 3.4%; Pred. No. 0.0081;
Matches 13; Conservative 219; Mismatches 155; Indels 0; Gaps 0;

Oy	191	GGAGCCGGAGGGAGCCATCGGGCGGAGCCAGGTTGGACCTTCTCCACAGCA	250
Db	1438	GTACRR	1379
Oy	251	AACGTGCTCTGGAGATCATCTGTAATTTAGTGAATGAAAAATCAGGTGAGTAC	310
Db	1378	RR	1319
Oy	311	TGGAAGATACCAAGCCAGTGGAACAGTGATTAAACAGTGAAGTTGTTAAGACGA	370
Db	1318	RR	1258
Oy	371	CATGCGCTTTACAGCTGGGAGTGCATCTCTTGTAACGGAAGATGAACCGGAC	430
Db	1258	RR	1199
Oy	431	ACAACGTGCATCCTCTATGATTTTAAAGTAAACAGGACGATGACAGATCT	490
Db	1198	RR	1139
Oy	491	TTGAAGCTAACAGGAAAATGTGTTCCATGGGACCAAGATACCTCAGTGCAGTGCA	550
Db	1138	RR	1079
Oy	551	GGCGAGGGCGGATCCCGGGCTCTC	577
Db	1078	RRRRRRRRRRATCGAAGCTCCCTC	1052

```

RESULT 2
US-09-621-976-16656
; Sequence 16656; Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCE: GENST. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16656
LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16656

```

Query Match	1.7%;	Score 46.2;	DB 4;	Length 430;
Best Local Similarity	17.4%;	Pred. No. 0.039;		
Matches 57;	Conservative 126;	Mismatches 144;	Indels 0;	Gaps 0;

Qy	1528	GGAAGCACCGCCCTGTGACACTGTGCCTTCAGGCCAATGCCGACCGGAGAGCGGAGGGC	1587
Db	56	SGRAMCCYTYKKKSSCSBAMCCCCCTTYTKSCSSYKSYSYTTAKAMMKRRKSLTYSERR	115
Qy	1588	GAGCAGAGACC CGCGTGTCGCCCTTAGCAGTGATGTGCGATCTGCTCGACGCTTTCTGCCAC	1647
Db	116	MYYYRSMYYMRSMWKGSCCCS GGS CYKKKKKKKGSCCMRSYWMCCYYYKRARRMMWK	175
Qy	1648	CTGTACTGGGGCTCACCCGGGACCGGCGTCTAACGGCTGCTGGGCCCGTTTYTGAGGCTC	1707
Db	176	GGS CMYTKRMWRMRMCCCMRRSRMRMRMCMWGSYTYCYKSSSNMCMARMRARSKK	235
Qy	1708	AACCTGGGTGACAAGTGTCTGACGCGCGTGTCTGAACAACAACACTCAAGATCAGAATC	1767
Db	236	RMCYTITGGGGMWRYCMCRKKGRRACTGTTCACCTGCCCGTGTCTGCGAAGAGCCCTTC	295
Qy	1768	CTGAAGAAATTACTGGCAACGAGAGTTTGACATGAAAAAACATGTTGACCGAGAGCCTC	1827

Db 296 ACCTACACCGCATGTGKAMCSCMMMKRRPKKKTKMMAMSRMSTKARRRRSGMTCYY 355

Qy 1828 GTGCTCTCCAGCGGAGAGTGTTCG 1854

Db 356 KSMMSKMYTKSSGGRAGGCTTCAATG 382

```

RESULT 3
US-09-807-258-13
: Sequence 13, Application US/09807258
: Patent No. 6670166
: GENERAL INFORMATION:
: APPLICANT: E. I. du Pont de Nemours and C
: TITLE OF INVENTION: Arthropod Protein Dis
: FILE REFERENCE: BB-1253 PCT
: CURRENT APPLICATION NUMBER: US/09/807,258
: CURRENT FILING DATE: 2001-06-11
: PRIORITY APPLICATION NUMBER: 60/104,376
: PRIOR FILING DATE: 1998-10-15
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 13
: LENGTH: 1759
: TYPE: DNA
: ORGANISM: Scolopendra canidens DS
: US-09-807-258-13

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Query Match	1.7%;	Score 45.8;	DB 4;	Length 1759;
Best Local Similarity	49.4%;	Pred. No. 0.11;		
Matches 119; Conservative	0;	Mismatches 122;	Indels 0;	Gaps 0;

QY	2439	AGGAAAAGTTTCAAGGGAGAAGGCCAAGTTATCATAAAAACATTGTTCAGAGGAAGGAG	2498
Dd	1514	AGAAAAAAGTTGAAITTTGAATAGTAGCAITTTAGAAITTTAAATATTTTGCTCAGTAATAAGC	1573
QY	2499	CATTAAGTTACAGCGTACAGAACGTACAATATCTCGCTCGGAGAAACACAGCATT	2558
Dd	1574	ACAATTTTTTATTTTAAAGGAATAAAAATGTAATAAATCAATATATGATTAATTAATAATT	1633
QY	2559	TTATCTATTTTTTATTTTAAATAGTTTGGTGCTTATCTCTGAATTAAGTTTAAATGTCAAC	2618
Dd	1634	AGAGTGCTTATGTTGGTGGACGTATGCTTATTTCTTTGTGAAGTAATAAAGTTGAA	1693
QY	2619	AAACTGACACAATAATATTAATTTTAAATTTTCAAAATGTGACAAAAAATTTTTTTTTT	2678
Dd	1694	AATTAATTCGAATTAATAATTTTTTTTAAATATAGTTTTCACAAAAGCAAAAAAAAAAAAA	1753
QY	2679	A 2679	
Dd	1754	A 1754	

RESULT 4
US-08-924-747-25
Sequence 25, Application US/08924747
Patent No. 6063570
GENERAL INFORMATION:
APPLICANT: MCCONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,747
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
US-08-924-747-25

Query Match 1.7%; Score 45.4; DB 3; Length 991;
Best Local Similarity 51.2%; Pred. No. 0.099;
Matches 106; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2473 AAAAATTGTTTCAGAGAGAGAGATTAAGTTTACAGCTTACAGAGCTACAAATAT 2532
DB 766 AGAACATTTTGAAGGTAGATTCATTAATAGTAGATTTTGTGGAAACAATTA 825
QY 2533 CCTGCTGCTGGGAAACACAGCATTTTATCTATTTTAAATTAAGTTGGTCTT 2592
DB 826 TCTTGTGAGCAAGAGATTTGCTGTTTAAATTAATTAATGCTGATTTGGTGGT 885
QY 2593 ATCTTCTAATAGATTTAAATGTCACAACTGTAGACAAATTAATTAATTAATTA 2652
DB 886 ATGGCTATTTTAATTTAACTAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAA 945
QY 2653 CAAATGACAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAAAGAGTTC 2679
DB 946 AAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAA 972

RESULT 5
US-09-247-373B-25
Sequence 25, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 991
TYPE: DNA
ORGANISM: SOYBEAN
US-09-247-373B-25

Query Match 1.7%; Score 45.4; DB 3; Length 991;
Best Local Similarity 51.2%; Pred. No. 0.099;
Matches 106; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2473 AAAAATTGTTTCAGAGAGAGAGATTAAGTTTACAGCTTACAGAGCTACAAATAT 2532
DB 766 AGAACATTTTGAAGGTAGATTCATTAATAGTAGATTTTGTGGAAACAATTA 825
QY 2533 CCTGCTGCTGGGAAACACAGCATTTTATCTATTTTAAATTAAGTTGGTCTT 2592
DB 826 TCTTGTGAGCAAGAGATTTGCTGTTTAAATTAATTAATGCTGATTTGGTGGT 885
QY 2593 ATCTTCTAATAGATTTAAATGTCACAACTGTAGACAAATTAATTAATTAATTA 2652
DB 886 ATGGCTATTTTAATTTAACTAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAA 945
QY 2653 CAAATGACAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAAAGAGTTC 2679
DB 946 AAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAAAAGAGTTCAGTTTAAAA 972

RESULT 6
US-09-296-715-25
Sequence 25, Application US/09296715
Patent No. 6171839
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSER: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,715
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEtical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
US-09-296-715-25

Query Match 1.7%; Score 45.4; DB 3; Length 991;
Best Local Similarity 51.2%; Pred. No. 0.099;
Matches 106; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 2473 AAAAATTGTTTCAGAGAGAGAGATTAAGTTTACAGCTTACAGAGCTACAAATAT 2532
DB 766 AGAACATTTTGAAGGTAGATTCATTAATAGTAGATTTTGTGGAAACAATTA 825

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QY 2533 CCTGCTGCTGGGAAACCAAGCATTATCTATTTTATTTTATAGTTGCTT 2592
DB 826 TCTTGTGTGAGCAAGATGTTCTGTTTAAATTAATGATGTTGTTGGT 885
QY 2593 ATCTTATTAAGATTAATGTCACAACTGTAGACAAATTAATTAATTA 2652
DB 886 ATGGGTATTTTAAATTTTAACTAAATAAGTGTGATTAAATAAAAAA 945
QY 2653 CAATTGACAAAAAATTTTAAAAA 2679
DB 946 AAAAAAAAAAAAAAAAAAAAAA 972

RESULT 7
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 1.7%; Score 45.2; DB 3; Length 4403765;
Matches 101; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 32 GACACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 91
DB 3793359 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3793418
QY 92 TGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 151
DB 3793419 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3793478
QY 152 GTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 211
DB 3793479 GRCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3793538
QY 212 GCGCGAGACGAGT 225
DB 3793539 GCGCGCGCGCGCGT 3793552

RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
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; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 1.7%; Score 45.2; DB 3; Length 4411529;
Matches 101; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 32 GACACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 91
DB 3802537 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3802596
QY 92 TGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 151
DB 3802597 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3802656
QY 152 GTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 211
DB 3802657 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3802716
QY 212 GCGCGAGACGAGT 225
DB 3802717 GCGCGCGCGCGCGT 3802730
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RESULT 9
US-10-140-002-321
; Sequence 321, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gettisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 321
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-321

Query Match
Best Local Similarity 1.6%; Score 42.8; DB 4; Length 783;
Matches 86; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2522 GTACACATATTCGCTGCTGGGAAACACAGCATTTATTTTATTTATAG 2581
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Db 625 GAAGCTACATGAGCCCGTGGGAGAGAGGGTGTTCCTCCAGATTACTTAATA 684
 QY 2582 GTTGGTGTCTATCTCTATATAGATTTAATGTGACAACTGTAGCACAATAATATA 2641
 Db 685 AGCTTGTATAGATTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 744
 QY 2642 TTTATATTACAAATTGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2679
 Db 745 AA 782

RESULT 10

US-08-910-925-2/c
 ; Sequence 2, Application US/08910925
 ; Patent No. 6162601
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN PININ SPLICE VARIANT
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: PastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/08/910,925
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0365 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: FIBERNOT01
 ; CLONE: 53219
 ; US-08-910-925-2

Query Match 1.6%; Score 42.6; DB 3; Length 2369;
 Best Local Similarity 58.1%; Pred. No. 0.83;
 Matches 75; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1639 TTCTGCACCTGTACTGAGGAGTGCACCCGAGCCGCTGTACGGCTGCTGCGCCCGTTT 1698
 Db 1873 TGTGTGACCTGTACTGAGGAGTGCACCCGAGCCGCTGTACGGCTGCTGCGCCCGTTT 1814
 QY 1699 TGTGACTCAACTGGGTGACAGAGTGTGACGGGCTGTGAACAACAAGCTACGAG 1758
 Db 1813 TGTAACTACTTCCACTGCTGTACTGCTGTTGAAGTGTACTGAACGCTACTACTGCTC 1754
 QY 1759 TCAGACATC 1767

Db 1753 TTGACTTC 1745

RESULT 11

US-09-252-991A-2236/c
 ; Sequence 2236, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 2236
 ; LENGTH: 966
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-2236

Query Match 1.6%; Score 42.4; DB 4; Length 966;
 Best Local Similarity 54.5%; Pred. No. 0.58;
 Matches 85; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 74 CGGGATGTGATCCCGATGAGCGGCCGAGAGGAGCAAGCATGCTCCGCCGCGCAGC 133
 Db 578 CGCTGCTGTATCCGATCGATCGATCGCTGACGACAAAGAGAGCGCTGGCGGAGG 519
 QY 134 CCGGGAGCGCTCTGCGTCTGCGGCGGAGAGAGCGGAGCGGACGCTCTCTGAGGA 193
 Db 518 CCGTGGGCGGCTCGCGAGAGCGGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGG 459
 QY 194 AGCGGAGTGCACCATCGGCGGAGAGAGGAGGTTGCG 229
 Db 458 AGCATCGGCTGCTGATCGGCTATGCGCGGCGGTTGGCG 423

RESULT 12

US-09-252-991A-2607
 ; Sequence 2607, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 2607
 ; LENGTH: 1734
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-2607

Query Match 1.6%; Score 42.4; DB 4; Length 1734;
 Best Local Similarity 54.5%; Pred. No. 0.79;
 Matches 85; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 74 CGGGATGTGATCCCGATGAGCGGCCGAGAGGAGCAAGCATGCTCCGCCGCGCAGC 133
 Db 1212 CGCTGCTGTATCCGATCGATCGGCTGACGACAAAGAGAGCGGCGCTGGCGGAGG 1271
 QY 134 CCGGGAGCGCTCTGCGTCTGCGGCGGAGAGAGGAGGTTGCG 193

DB 1272 CCGCTGGCGGGCTCCCGGAGATCCCGGCGAGAGCACTGCGCCGCGGATCTCGAGCGCG 1331
QY 194 AGCGGAGTGAACCATCGGCGGAGACGAGGTTGCG 229
DB 1332 AGCATGCGGTGCTGATCGGTCAATGCGCGGTTGCG 1367

RESULT 13
US-09-252-991A-2445
Sequence 2445, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2445
LENGTH: 2016
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2445

Query Match
Best Local Similarity 54.5%; Score 42.4; DB 4; Length 2016;
Matches 85; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 74 CGGGATGTGAATCCGATGAGCGCGCGGAGAAAGCAAGATCGCGCGCGCGCAGC 133
DB 1454 CGCTCTGTTCATCCGATCGATCGCTGCGACAAAGGAGGAGCGCTGGCGGAGG 1513
QY 134 CTTGGGAGCGCTCTGCGCTCTGGGCGGAGAGAGGCGGAGCGGACGTCCTCTGAGGA 193
DB 1514 CCGCTGGCGGGGCTCGCGGAGATCGCGGAGGAGCGGAGCGGCGGATCTCTGAGCGG 1573
QY 194 AGCGGAGTGAACCATCGGCGGAGACGAGGTTGCG 229
DB 1574 AGCATGCGGTGCTGATCGGTCAATGCGCGGTTGCG 1609

RESULT 14
US-10-204-708-62/c
Sequence 62, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIERENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 62
LENGTH: 6801

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-62

Query Match
Best Local Similarity 58.9%; Score 42.4; DB 4; Length 6801;
Matches 73; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 2556 ATTTATATATTTTATTTTATATAGTTGGTCTATCTTCAATAGATTAAATGT 2615
DB 2997 ATTAATCAACTTTTCTTTTACTTATATCTTTTATATATATATATATATAT 2938
QY 2616 CACAACTGTGCAAAATATATATATTTATTTACAAATTGACAAAAAATAA 2675
DB 2937 ATTTCACCTAAACAAATTAATATATATATATATATATATATATATATAT 2878
QY 2676 AAAA 2679
DB 2877 AAAA 2874

RESULT 15
US-09-790-988-1
Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: MATANABE, HIDEKI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 64081
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match
Best Local Similarity 50.5%; Score 42.4; DB 4; Length 64081;
Matches 103; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2464 AAGTTATCAAAAACATTTGTTTCAGGAGGAGGAGCATTAATTACAGCCTACAGAGCT 2523
DB 625138 AAGGCTATCTATTATTAACAAATTTATTTAAAGTATATTTACATGCGCTTCAT 625197
QY 2524 ACACATATCTGCTGCGGAGAAACAGCATTTATCTATTTTATTTATATAGT 2583
DB 625198 GCAAAATTTATGCAATTTGAGAAAGAGCATGCTCTTTTCTTTTATATATATAT 625257
QY 2584 TTGGTCTTATCTTCAATAGATTTAAGTCAACAACTGTACACAAATATATATTT 2643
DB 625258 AATTTATTTTCTTAAATATATATATATATATATATATATATATATATAT 625317
QY 2644 TATATTTTCAAAATTGACAAAAA 2667
DB 625318 ACAAATTAAT 625341

Search completed: January 15, 2005, 06:21:34
Job time : 234 secs

US-10-108-260A-2073

Query Match 71.6%; Score 1919.4; DB 16; Length 2448;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 2227; Conservative 0; Mismatches 6; Indels 284; Gaps 2;

QY 218 GACGAGGTTGCGACCTTTCTCCCGACGAAATTAATCTGTCTCTGGAGATCACTGTAGAA 277
DB 83 GACCCGTGTGCGACCTTTCTCCCGACGAAATTAATCTGTCTCTGGAGATCACTGTAGAA 142

QY 278 TTGTAGTGAATGAAAATCAAGTCAAGTGAACACTGTGAAGATACACGACCACTGGAACAG 337
DB 143 TTGTAGTGAATGAAAATCAAGTCAAGTGAACACTGTGAAGATACACGACCACTGGAACAG 202

QY 338 TGAATTAACAAGCTGAAGGTTGTGTTAAGACGACATGCCCCCTTACGACTGGGGAGTGA 397
DB 203 TGAATTAACAAGCTGAAGGTTGTGTTAAGACGACATGCCCCCTTACGACTGGGGAGTGA 262

QY 398 TCTACTTGTGTACAGAGAAATGACCGGAAACACACAGTGGCATCTCTAATGAACTTT 457
DB 263 TCTACTTGTGTACAGAGAAATGACCGGAAACACACAGTGGCATCTCTAATGAACTTT 322

QY 458 TAAAGTAAAGCAAGGCAATGACACAGAAATCTTTGAAGCTAACAGAAAATGTGTTCC 517
DB 323 TAAAGTAAAGCAAGGCAATGACACAGAAATCTTTGAAGCTAACAGAAAATGTGTTCC 356

QY 518 ATGGGACCAAAAGATACCTCAAGGTGACAGGTGACAGGGGCGAGGGCCGATCCCGGGTCCCTC 577
DB 357 ----- 356

QY 578 CGTCGTGCGCCGCACTCAAGTGTGCTTTAGAGAACACAGCCATCAATGACGTGAG 637
DB 357 ----- 356

QY 638 ACCCTTCCCAACAGCCTCGGCCTCTTCCACGAGAGCTTCTCTGAGGGCGAGAGCTTT 697
DB 357 ----- 356

QY 698 CCTCCAGTTGTGGGTGTGGGGGTGTGGCATCTCCCTTAAGAAATGTGTTCTCTGTGG 757
DB 357 -----TGGGTGTGGGGGTGTGGCATCTCCCTTAAGAAATGTGTTCTCTGTGG 406

QY 758 CAAGTATGAAGTCTCAGCTTTGCTCAGCTCTCCAGACAGAAAGATCGGTCTCTTT 817
DB 407 CAAGTATGAAGTCTCAGCTTTGCTCAGCTCTCCAGACAGAAAGATCGGTCTCTTT 466

QY 818 CGTCGTGGAACCCCAAGATCAAGAGATTTGAGCCCGTGAAGAAATGAGAGAG 877
DB 467 CGTCGTGGAACCCCAAGATCAAGAGATTTGAGCCCGTGAAGAAATGAGAGAG 526

QY 878 ATGGGACCTTGAACCTGAACCGGCAATTTGTGTGCGACACACCGGTAGAAATGCCA 937
DB 527 ATGGGACCTTGAACCTGAACCGGCAATTTGTGTGCGACACACCGGTAGAAATGCCA 586

QY 938 CGTCACAGAGACGTCAAGACAGCGGCTGGGAGCGACAGAAAGTGAAGAGAGCGCTGA 997
DB 587 CGTCACAGAGACGTCAAGACAGCGGCTGGGAGCGACAGAAAGTGAAGAGAGCGCTGA 646

QY 998 CATGATCATCTGCGAGGACCTGTCTGACAGCTGCTGAGTTTGAAGCCCTGATGACACA 1057
DB 647 CATGATCATCTGCGAGGACCTGTCTGACAGCTGCTGAGTTTGAAGCCCTGATGACACA 706

QY 1058 CGTTTCCGCGGCTTGTACTGTGGGCTGGATGAGAGCGCTGCTGTCTCTAAGCTGCT 1117
DB 707 CGTTTCCGCGGCTTGTACTGTGGGCTGGATGAGAGCGCTGCTGTCTCTAAGCTGCT 766

QY 1118 GCGTGCCTGGAGCGGATCTGTAAACACATCTCTCAACAACTCGTGAAGACATAC 1177
DB 767 GCGTGCCTGGAGCGGATCTGTAAACACATCTCTCAACAACTCGTGAAGACATAC 826

QY 1178 TCATCCAGATCCAGACAAAGATGCGAGTGAAGAAAGATGCAAGTATGATGCCAGGA 1237
DB 827 TCATCCAGATCCAGACAAAGATGCGAGTGAAGAAAGTATGATGCCAGGA 886

QY 1238 ATAAATCACTCAAGACATGCTGACGAGCCCAAGTCAAGGCGGTCTTTCTGATGAAGAG 1297
DB 887 ATAAATCACTCAAGACATGCTGACGAGCCCAAGTCAAGGCGGTCTTTCTGATGAAGAG 946

QY 1298 GAGGTTCAAGAGACCTGCTGAGCTGTCAAGCTTGAACAGTATGCTCTGACATTTAGCC 1357
DB 947 GAGGTTCAAGAGACCTGCTGAGCTGTCAAGCTTGAACAGTATGCTCTGACATTTAGCC 1006

QY 1358 AACCATACGTGCTGTGCGCGAGTGTCTGAGTACAGAAAGGACGCGCGACCTCC 1417
DB 1007 AACCATACGTGCTGTGCGCGAGTGTCTGAGTACAGAAAGGACGCGCGACCTCC 1066

QY 1418 ACTGCCAGACACCCAGAGCGCGACAGAGACCCCAAGGCTCTGGGGAGTGAACCTTCA 1477
DB 1067 ACTGCCAGACACCCAGAGCGCGACAGAGACCCCAAGGCTCTGGGGAGTGAACCTTCA 1126

QY 1478 CGTCGTCAGCTGACGACAGCATGTCAGAGATTAAGTGTGCCCTCTGCAAGGAGCAG 1537
DB 1127 CGTCGTCAGCTGACGACAGCATGTCAGAGATTAAGTGTGCCCTCTGCAAGGAGCAG 1186

QY 1538 CCTGTGACCTGTGCTTCCAGCCCATGCGGACCGGAGAGCGGACGCGACAGACC 1597
DB 1187 CCTGTGACCTGTGCTTCCAGCCCATGCGGACCGGAGAGCGGACGCGACAGACC 1246

QY 1598 CGCGTGTGCGCCCTGACAGATGTGGGTGTGCTGCTGACAGCTTTCTGACCTGTACTGG 1657
DB 1247 CGCGTGTGCGCCCTGACAGATGTGGGTGTGCTGCTGACAGCTTTCTGACCTGTACTGG 1306

QY 1658 GCTGACCCGAGACCGGCTGTACGGCTGCTGAGCCCTGTTTGT-----GAGCTCA 1701
DB 1307 GCTGACCCGAGACCGGCTGTACGGCTGCTGAGCCCTGTTTGTGTGTGTGCGGACAGACT 1366

QY 1702 -----GAGCTCA 1709
DB 1367 GCTTCTGCGACATCATTAATAACAGGTAACTATGCCCTTCATCTGCGGACAGCTCA 1426

QY 1710 CCTGGGTGACAGTGTCTGAGACGGGTGTGTAACAACAACAGCTACAGTCAATCT 1769
DB 1427 CCTGGGTGACAGTGTCTGAGACGGGTGTGTAACAACAACAGCTACAGTCAATCT 1486

QY 1770 GAAAGATTAACCTGGAACAACAGAGTTTGAATGAGAAAAATGTGACCGAGCTCGT 1829
DB 1487 GAAAGATTAACCTGGAACAACAGAGTTTGAATGAGAAAAATGTGACCGAGCTCGT 1546

QY 1830 GGCCTTCCAGCGGGAGTGTCTGTCTGTGATTAACAGAGTCAACGGAGACACCTTCT 1889
DB 1547 GGCCTTCCAGCGGGAGTGTCTGTCTGTGATTAACAGAGTCAACGGAGACACCTTCT 1606

QY 1890 GTTTACTGTGTGCTGCGGACGCTTCCGTGAGCTGACCTATCATGTATCGGACAAACT 1949
DB 1607 GTTTACTGTGTGCTGCGGACGCTTCCGTGAGCTGACCTATCATGTATCGGACAAACT 1666

QY 1950 TCCCTGCTCCGAGTTGCCAGTGGCCGTAAACATCCCGTCTGTACTGTGGGCGGTAA 2009
DB 1667 TCCCTGCTCCGAGTTGCCAGTGGCCGTAAACATCCCGTCTGTACTGTGGGCGGTAA 1726

QY 2010 CTGCGCACTCAGTGAAGGCTCAACAGCCATGAATTAATCATATCTGTGAACAGAC 2069
DB 1727 CTGCGCACTCAGTGAAGGCTCAACAGCCATGAATTAATCATATCTGTGAACAGAC 1786

QY 2070 AAGGTTCAAAAATTAAGCATCCAGAGGCGCTGAGCAAGCTTTGACGACTGGAAGTAAAG 2129
DB 1787 AAGGTTCAAAAATTAAGCATCCAGAGGCGCTGAGCAAGCTTTGACGAGTAAAG 1846

QY 2130 AGCGTGTGTTTAAATTAAGAGACAAGACCGTCAAGGTGTTTTCAGAGCCCTGAGGGA 2189
DB 1847 AGCGTGTGTTTAAATTAAGAGACAAGACCGTCAAGGTGTTTTCAGAGCCCTGAGGGA 1906

QY 2190 AAGGACGAGGCTCTCCAGACAGTGTCTGTGGGTGACTCTTCTGTGAGACTTTTAACT 2249
DB 1907 AAGGACGAGGCTCTCCAGACAGTGTCTGTGGGTGACTCTTCTGTGAGACTTTTAACT 1966

[illegible]

RESULT 3
US-09-764-864-22

```

Sequence 22, USApplication US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
  APPLICANT: Rosen et al.
  TITLE OR INVENTION: Nucleic Acids, Proteins, and Antibodies
  FILE REFERENCE: PT723
  CURRENT APPLICATION NUMBER: US/09/764,864
  PRIOR FILING DATE: 2001-01-17
  Prior application data removed - consult PALM or file wrapper
  NUMBER OF SEQ ID NOS: 1792
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 22
  LENGTH: 1311
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
    NAME/KEY: SITE
    LOCATION: (1281)
  OTHER INFORMATION: n equals a,t,g, or c
  US-09-764-864-22

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Query Match	35.3%;	Score 945;	DB 9;	Length 1311;
Best Local Similarity	81.1%;	Pred. NO. 1.7e-243;		
Matches 1267;	Conservative	6;	Mismatches 7;	Indels 282;
				Gaps 4

Qy	50	TCGGGGTTGGCGCGCGGGGGGGGGATGTGAATCCGACATGAGCGCCGAGGAAGCGAAGC	115
Db	5	TCGGGGTTGGCGCGCGGGGGGGGGATGTGAATCCGATGAGCGGCCGAGGAAGCGAAGC	64
Qy	116	AGTCGCGCGCGCGCGACGCGCTGTGGGACCGACTTCCTGGGCGCGGAGGGGCGAGC	1751
Db	65	AGTCGCGCGCGCGCGACGCGCTGTGGGACCGACTTCCTGGGCGCGGAGGGGCGAGC	124
Qy	176	CGACGTCCTCTCTGAGGAAGCGGAGTGGACCATGTGGGCGGAGACAGAGTTGGCACTTT	225
Db	125	CGACGTCCTCTCTGAGGAAGCGGAGTGGACCATGTGGGCGGAGACAGAGTTGGCACTTT	184
Qy	236	CCCTCCGACGATTAACGTCTCTGAGAGTCACTGATGATTGTAGTGATGAAAAAT	295
Db	185	CCCTCCGACGATTAACGTCTCTGAGAGTCACTGATGATTGTAGTGATGAAAAAT	244
Qy	296	CAGTCAGTGACACTGGAAAGATCCAGACCAAGTGGAAAGATGATTAAACAAGCTGAAG	355

Db	245	CAGGTGAGTGA	CACTGGAA	AGATACCA	GCACCA	CCAGTGGAA	CAGTGA	TTTAACAA	CTGA	ARG	304
Oy	356	TTGTTAAGAA	GCAGACAT	CGCCCTTTA	CACAGCT	GGGATGT	CACTACT	TGTGTGA	CAGA	415	
Db	305	TTGTTAAGAA	RCAGACAT	CGCCCTTTA	CACAGCT	GGGATGT	CACTACT	TGTGTGA	CAGA	364	
Oy	416	AGAA	TGAACCGGAA	CA	CAAGTGG	CACTCTAT	TGATCTTTAA	AGGAAACAG	AGCA	475	
Db	365	AGAA	TGAACCGGAA	CA	CA					382	
Oy	476	TGACACA	AGAATCCTTTGA	AGTTAACAG	AAAAATG	TTTCCAT	TGAGGACCA	AAATAC	TACT	535	
Db	383	-----								382	
Oy	536	CAGGTGAGT	GACAGGCGAGGGG	CGATCCCGGGT	CCTCCGT	CGTGC	CCCGCA	CTC		595	
Db	383	-----								382	
Oy	596	AGGTGCTTTG	AGAAACCA	CAGCCAT	CAACAT	GACGT	ACAG	CTTTCCCA	CAGCT	655	
Db	383	-----								382	
Oy	656	CGGCTCTT	CCACGAGACCTT	CTC	TGACAGGCGAG	AGCTT	CTC	CA	GT	715	
Db	383	-----								382	
Oy	716	GGGGTGTG	GCATCTCCCTTAA	AGAAATG	GTCTCTT	TGCGA	AGTGA	AGTCC	CA	775	
Db	389	GGGGTGTG	GCATCTCCCTTAA	AGAAATG	GTCTCTT	TGCGA	AGTGA	AGTCC	CA	448	
Oy	776	GCTTTGCTT	CAGCTCTCTCC	CAGACAGAA	AGCTGCTCTTTT	GTGCTG	TGAAACCC	AGG		835	
Db	449	GCTTTGCTT	CAGCTCTCTCC	CAGACAGAA	AGCTGCTCTTTT	GTGCTG	TGAAACCC	AGG		508	
Oy	836	ATCAGAGAT	TTTGAGACCCG	TGAAAGAAAT	TGAGAGAGAT	GGGACCTT	GACCTGA			895	
Db	509	ATCAGAGAT	TTTGAGACCCG	TGAAAGAAAT	TGAGAGAGAT	GGGACCTT	GACCTGA			568	
Oy	896	ACGGGCA	GTGTTG	TGTCGACAA	CCGCGTAGAAAT	GGCCAA	CCGTCC	CACGAGAG	CGTCA	955	
Db	569	ACGGGCA	GTGTTG	TGTCGACAA	CCGCGTAGAAAT	GGCCAA	CCGTCC	CACGAGAG	CGTCA	628	
Oy	956	GAGCAG	CGCGCTGG	AGAACCCAGACAA	AGATGAGAGAG	AGCTGACAT	GATATCT	GTCC	AGG	1015	
Db	629	GAGCAG	CGCGCTGG	AGAACCCAGACAA	AGATGAGAGAG	AGCTGACAT	GATATCT	GTCC	AGG	688	
Oy	1016	ACCTGCG	CA	CGACTGCGTGA	GGCTGACCGCTG	CA	CGATTC	TGCGCGG	CTGCT	1075	
Db	689	ACCTGCG	CA	CGACTGCGTGA	GGCTGACCGCTG	CA	CGATTC	TGCGCGG	CTGCT	748	
Oy	1076	ACTCGGG	CTGGAT	TGAGCGCTG	CTCTGTCTCTA	CTTG	CCGCTG	CTCCG	TGAGCGGA	1135	
Db	749	ACTCGGG	CTGGAT	TGAGCGCTG	CTCTGTCTCTA	CTTG	CCGCTG	CTCCG	TGAGCGGA	808	
Oy	1136	TCGTGTAAA	AAACCA	CATCTCTCA	CAACCTCGT	TGAGAGAT	CACTCAT	CACAGT	TC	1195	
Db	809	TCGTGTAAA	AAACCA	CATCTCTCA	CAACCTCGT	TGAGAGAT	CACTCAT	CACAGT	TC	868	
Oy	1196	AGATG	GCACATG	GAAGAGAT	GTGCAAA	GTATGAT	GCAGAA	TTAAAT	CACTCA	1255	
Db	869	AGATG	GCACATG	GAAGAGAT	GTGCAAA	GTATGAT	GCAGAA	TTAAAT	CACTCA	928	
Oy	1256	TGCTGCA	AGCCCA	AGTCAG	CGGCTCTTTTCTG	TGAGAA	AGGAGAT	TTCAGAG	ACCTGC	1315	
Db	929	TGCTGCA	AGCCCA	AGTCAG	CGGCTCTTTTCTG	TGAGAA	AGGAGAT	TTCAGAG	ACCTGC	988	
Oy	1316	TGAGCTGT	CA	CACTGTGA	CA	GTGAGTCTT	CA	CATTAG	CCACCAT	1375	
Db	989	TGAGCTGT	CA	CACTGTGA	CA	GTGAGTCTT	CA	CATTAG	CCACCAT	1048	
Oy	1376	GGCAGT	CTCTG	ATACAG	AGGAGGCGG	CGACCTT	CCCACT	GGCCAG	CA	1435	


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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (623)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (640)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (670)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (687)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (690)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-483

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Query Match 20.0%; Score 536.6; DB 9; Length 693;

Best Local Similarity 92.5%; Pred.No. 1.3e-133;

Matches 608; Conservative 7; Mismatches 13; Indels 29; Gaps 4;

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QY 1044 GCCCTGATGACAGCTTCTGCGCGCTTGTACTCGGGCTGAGAGCGCTCGTCCCT 1103
DB 14 GCCCTGATGACAGCTTCTGCGCGCTTGTACTCGGGCTGAGAGCGCTCGTCCCT 73
QY 1104 GTGTCTTACCTGCGCTGTCTCGGTGAGCGGATCTGTAAACCAATCTTCAACACT 1163
DB 74 GTGTCTTACCTGCGCTGTCTCGGTGAGCGGATCTGTAAACCAATCTTCAACACT 133
QY 1164 CGTGAAGCATCTCATCAGCATCCAGAGAGTGGAGTGAAGAGATGTGCAAG 1223
DB 134 CGTGAAGCATCTCATCAGCATCCAGAGAGTGGAGTGAAGAGATGTGCAAG 193
QY 1224 TATGATGCGAAGAAATAAATCACTCAAGACATGCTGAGCCCAAGTCAAGCGCTCTT 1283
DB 194 TATGATGCGAAGAAATAAATCACTCAAGACATGCTGAGCCCAAGTCAAGCGCTCTT 253
QY 1284 TTCTGATGAAGAGAGATTCAGAGAGCTGCTGAGCTGTGACGTTGACATGATG 1343
DB 254 TTCTGATGAAGAGAGATTCAGAGAGCTGCTGAGCTGTGACGTTGACATGATG 313
QY 1344 CTCAGACATTAAGCCAGCCATAGTGTGCGGAGTGTCTGAGTACAGAGGCGAGC 1403
DB 314 CTCAGACATTAAGCCAGCCATAGTGTGCGGAGTGTCTGAGTACAGAGGCGAGC 373
QY 1404 GCGGAGAGCTTCCCACTGCGGAGCAAGCCGAGGCGAGGCGAGGCGAGGCGAGG 1463
DB 374 GCGGAGAGCTTCCCACTGCGGAGCAAGCCGAGGCGAGGCGAGGCGAGGCGAGG 433
QY 1464 GATATGACCTTCCAGCTGCTGAGCTGAGCAGACAGAGTTCAGGATTCGTTGCTCT 1523
DB 434 GATATGACCTTCCAGCTGCTGAGCTGAGCAGACAGAGTTCAGGATTCGTTGCTCT 489
QY 1524 GCAAGGAAGCCAGCGCTGTGAGCACTGCTTCCAGCCAGCCAGGAGCGGAGCGGA 1583
DB 490 GCAAGGAAGCCAGCGCTGTGAGCACTGCTTCCAGCCAGCCAGGAGCGGAGCGGA 548
QY 1584 GCGGAGAGCAAGCCGCGGTGTGCGCCCTCAGACAGTGTGCGGTGCTGAGCGCTTCTG 1643
DB 549 -CGGAGAGCAAGCCGCGGTGTGCGCCCTCAGACAGTGTGCGGTGCTGAGCGCTTCTG 584
QY 1644 CCACTGTACTGTGGGCTGCAAGCCGAGCGGCTGCTAGCGGCTGCTGCGGCTTTTG 1700
DB 585 CCACTGTACTGTGGGCTGCAAGCCGAGCGGCTGCTAGCACTGCTGCGGCTTTTNG 641

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RESULT 6

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US-09-918-995-2180
; Sequence 2180, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysreg, Inc.

```

```

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918, 995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2180
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1) ... (476)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2180

```

Query Match 14.7%; Score 394.4; DB 10; Length 476;

Best Local Similarity 96.7%; Pred.No. 2.2e-95;

Matches 413; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

```

QY 2046 ATTCAATCATCTCTGTGAAGACAGAGGTTCAAAATCAAGCATCCAGAGGCGCTGAGCA 2105
DB 52 ATTCAATCATCTCTGTGAAGACAGAGGTTCAAAATCAAGCATCCAGAGGCGCTGAGCA 111
QY 2106 GCTTTCAGACTGAGAGGTGAAGAGCGGTGTTTAAATACAGAGCAAGCAGTCAG 2165
DB 112 GCTTTCAGACTGAGAGGTGAAGAGCGGTGTTTAAATACAGAGCAAGCAGTCAG 171
QY 2166 GTGTTTTCAGAGGCGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2225
DB 172 GTGTTTTCAGAGGCGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 231
QY 2226 CTCTTCTGTGAGAGGTTTAACTCTGAGTGAAGACCTTCCAGAGGCGCGGAGGAGG 2285
DB 232 CTCTTCTGTGAGG--TTTAACTCTGAGTGAAGACCTTCCAGAGGCGCGGAGGAGG 289
QY 2286 GCCCGGCTCTGTGAGAGCGCTGAGGAGGCGCTGTGATGATCAGAGCAGAGCAGAG 2345
DB 290 GACCGGCTCTGTGAGAGCGCTGAGGAGGCGCTGTGATGATCAGAGCAGAGCAGAT 349
QY 2346 CTTTCTGTAAAGTCCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2405
DB 350 CTTTCTGTAAAGTCCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 409
QY 2406 CCGAACTACAGTTAAAGAGAGTGTGTTTTCAGAAAGTTTCAAGGAGAGAGGAGG 2465
DB 410 CCGAACTACAGTTAAAGAGAGTGTGTTTTCAGAAAGTTTCAAGGAGAGAGGAGG 469
QY 2466 GTTTATC 2472
DB 470 GTTTATC 476

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RESULT 7

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US-09-764-864-322
; Sequence 322, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764, 864
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 322
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens

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? FEATURE:
? NAME/KEY: SITE
? LOCATION: (272)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: SITE
? LOCATION: (300)
? OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-332

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Query Match	11.6%;	Score 310.2;	DB 9;	Length 357;
Best Local Similarity	97.7%;	Pred. No. 8.9e-73;		
Matches 345; Conservative	0;	Mismatches 5;	Indels 3;	Gaps 3;

OY	56	TCGAGGTTGCGGCGCGGGGCGGGGATGTGAATCCCATGAGCGCGCCGAGGAAGCAAGC	115
Db	5	TCGGGGTTGCGGCGCGGGGCGGGGATGTGAATCCCATGAGCGCGCCGAGGAAGCAAGC	64
OY	116	AGTCGCGCGCGCCGCGAGCCCTTGGGGAGCGCTCTGCGGTCTGGCGCGGAGAGAGGCGAGC	175
Db	65	AGTCGCGCGCGCCGCGAGCCCTTGGGGAGCGCTCTGCGGTCTGGCGCGGAGAGAGGCGAGC	124
OY	176	CGCAGTCTCTCTGAGGAGACGGGAGTGGACATCGGGCGGAGACGAGTTCGACCTTT	235
Db	125	CGCAGTCTCTCTGAGGAGAGCGGAGTGGACATCGGGCGGAGACGAGTTCGACCTTT	184
OY	236	CCTTCCCGCAGTAATACTGGTCTCTGGAGATCACTGTAGATTGTAGTGGATGAAAAT	295
Db	185	CCTTCCCGCAGTAATACTGGTCTCTGGAGATCACTGTAGATTGTAGTGGATGAAAAT	244
OY	296	CAGGTCAAGTGCACATGTGAAGATACAGACACAGTGGAACAGTATTAAACAAGCTGAAG	355
Db	245	CAGGTCAAGTGCACGTGAAGATACANACACAGTGGAACAGTATTAAACAACCTNAAAG	304
OY	356	TTG-TTTAAGAGCAGACATGCC-TTTACAGACT-GGGATGTACTTACTTG	405
Db	305	TTGTTTAAGAAAACAGCATGCCCTTTTACAGCTGGGGAGTGCATCTACTTG	357

RESULT 8
US-09-918-995-13662

```

? Sequence 13662, Application US/09918995
? Publication No. US20030073622A1
? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc.
? TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
? FROM VARIOUS CDNA LIBRARIES
? FILE REFERENCE: 20411-756
? CURRENT APPLICATION NUMBER: US/09/918,995
? CURRENT FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: US/09/235,076
? PRIOR FILING DATE: 1999-01-20
? NUMBER OF SEQ ID NOS: 38054
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 13662
? LENGTH: 449
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)...(449)
? OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13662

```

Query Match	10.2%	Score 273.6;	DB 10;	Length 449;
Best Local Similarity	98.6%;	Pred. No. 7.4e-63;		
Matches 276; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 2387 TTGCTCTTTGACATTTTCCGAACTACAGTTAAGCAGAGCTGTCTTTCAGGAAAG 2444
Db 34 TCGCTCTTTGACATTTTCCGAACTACAGTTAAGCGGAGTCTGTCTTCAGGAAATAG 93
QY 2447 TTTCAAGGAGAAAGGCAAGTTATTCAAAAACATTGTTCAGGAGAAAGGAGCATTAAGTT 2506

[illegible]

RESULT 9
US-09-764-864-323
; Sequence 323, Application US/09764864
; Patent No. US20020132753A1

```

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 323
LENGTH: 354
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (313)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-323

```

Query Match	9.6%	Score 256.4;	DB 9;	Length 354;
Best Local Similarity	93.3%	Pred. No. 2.8e-58;		
Matches 266; Conservative	1;	Mismatches 18;	Indels 0;	Gaps 0;

QY	221	GAGGTGGCACCTTTCTCTTCCCGACAAATAA	CTGGTCTCGGAGATCACTGTAATG	280
Db	27	GAAATTAAGGACCTGACTTCCCGCAGATAA	ACTGGTCTCGGAGATCACTGTAATG	86
QY	281	TAATGATGAAAAATCATGCTCAGGTGAC	CTGGAAATACAGACCAAGTGGAACTGA	340
Db	87	TAATGATGAAAAATCAAGGTCAAGGTGAC	CTGGAAATACAGACCAAGTGGAACTGA	146
QY	341	TTTAAACAAGCTGAAGTGTGTTAAGAAGACA	CATGCGCCTTTACAGACTGGGATGTCACT	400
Db	147	TTTAAACAAGCTGAAGTGTGTTAAGAAGACA	CATGCGCCTTTACAGACTGGGATGTCACT	206
QY	401	ACTTGTGTACAGAGAAATGAACCGGAACA	CAACGTGGCATACCTCTATGAATCTTTAA	460
Db	207	ACTTGTGTACAGAGAAATGAACCGGAACA	CAACGTGGCATACCTCTATGAATCTTTAA	266
QY	461	GTTGAATAAGCATGCTGACACAAATCTCTTT	GAAAGCTAACAAAG	505
Db	267	GTTGAATAAGCATGCTGACACAAATCTCTTT	GAAAGCTAACAAAG	311

RESULT 10 864-742
US-09-764-864-742
; Sequence 742 Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 742
LENGTH: 354
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (313)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-742

Query Match 9.6%; Score 256.4; DB 9; Length 354;
Best Local Similarity 93.3%; Pred. No. 2.8e-58;
Matches 266; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

QY 221 GAGGTGGACCTTCCCTCCAGCAATTAACGTGCTCTGGAGATCACTGTAATTTG 280
DB 27 GAGATAGGAGCCTGACTTCCCTCCGATTAACGTGCTCTGGAGATCACTGTAATTTG 86
QY 281 TAGTGATGATTAATCAAGTCAAGTCACTGTAATTAACGACCAAGTGAAGTGA 340
DB 87 TAGTGATGATTAATCAAGTCAAGTCACTGTAATTAACGACCAAGTGAAGTGA 146
QY 341 TTAACAGTGAAGTGTGTTAAGAACGACACATGCTCTTACAGCTGGGATGTCATCT 400
DB 147 TTAACAGTGAAGTGTGTTAAGAACGACACATGCTCTTACAGCTGGGATGTCATCT 206
QY 401 ACTTGCTGACAGAAATGAACCGGAAACAACAGTGGCATACTTATGATCTTTAA 460
DB 207 ACTTGCTGACAGAAATGAACCGGAAACAACAGTGGCATACTTATGATCTTTAA 266
QY 461 GTGAAGCAAGGATGACACAGAAATCTTTGAAGCTAACAAGG 505
DB 267 GTGAAGCAAGGATGACACAGAAATCTTTGAAGCTAACAAGG 311

RESULT 11

US-09-908-975-6220
Sequence 6220, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:

APPLICANT: SHOSHAN, AVI
APPLICANT: WASSERMAN, ALON
APPLICANT: MINTZ, ELI
APPLICANT: FAIGLER, SIMCHON
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6220
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-6220

Query Match 2.2%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1843 GGAGTGTTCCTGCTGCTGATTAAGAGTCAAGGAGACACCGTCTGTTACTGCTGT 1902
DB 1 GGAGTGTTCCTGCTGCTGATTAAGAGTCAAGGAGACACCGTCTGTTACTGCTGT 60

RESULT 12

US-10-021-323-7699
Sequence 7699, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:

APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 7699
LENGTH: 520
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3828-019-Q1-N6-D6
US-10-021-323-7699

Query Match 2.0%; Score 54.2; DB 17; Length 520;
Best Local Similarity 65.0%; Pred. No. 0.001;
Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 2557 TTTATGATTTTATTTATTTATAGTTGCTGCTATCTTATTAATGATTTAAATGTC 2616
DB 139 TTTATGATTTTATTTATTTATAGTTGCTGCTATCTTATTAATGATTTAAATGTC 198
QY 2617 ACAACGTGACCAATTAATTAATTTATTAATTTACAAATTTGCAAAAAAAAAA 2676
DB 199 AAAAAAAAAAAAAAAAAAAAAAAAAAGTAAATTTTAAAAAAAAAAAAAAAAAAAA 258

QY 2677 AAA 2679
DB 259 AAA 261

RESULT 13

US-10-424-599-95539
Sequence 95539, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 95539
LENGTH: 1255
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..
OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: PAT_MRT3847_57283C.1
US-10-424-599-95539

Query Match
Best Local Similarity 1.9%; Score 51.4; DB 16; Length 1255;
Matches 94; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 2515 ACAGACGTACCAATATCTGCTGCGGAAACACAGCATTTATCTAATTTTATT 2574
DB 858 ACATGGGTGAACCTTTACTGCGGTGTGAATTAAGCAACCTTGTATCTTATTTTC 917
QY 2575 TTAATAGTTGGTCTTATCTTCTAATTAAGATTAAAGTCAAACTGTAGCAAT 2634
DB 918 TTGCTAGTAATAGAGTGTCTTACTTCTAATAAAAAAAAAAAAAAAAAAAAA 977
QY 2635 AATATATTTAATTTTACAAATTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 978 AAA 1022

RESULT 14

US-09-814-353-18006
Sequence 18006; Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Little, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18006
LENGTH: 383.
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-353-18006

Query Match
Best Local Similarity 1.9%; Score 51; DB 10; Length 383;
Matches 78; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 2557 TTTATCTATTTTATTTAATAGTTGGTCTTATCTTCAATAGATTAAATGTC 2616
DB 116 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 175
QY 2617 ACAACTGTAGCAAAATATATTTAATTTAATTTGACAAAAA 2676
DB 176 AAA 235
QY 2677 AAA 2679
DB 236 AAA 238

RESULT 15
US-10-424-599-127666/c

Sequence 127666; Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 127666
LENGTH: 411

TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_86287C.1
US-10-424-599-127666

Query Match
Best Local Similarity 1.9%; Score 51; DB 16; Length 411;
Matches 78; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 2557 TTTATCTATTTTATTTAATAGTTGGTCTTATCTTCAATAGATTAAATGTC 2616
DB 216 TCTTATCAATTTTGTGTTGGTGTGTATTTGTTGTTTAACTTTA 157
QY 2617 ACAACTGTAGCAAAATATATTTAATTTAATTTGACAAAAA 2676
DB 156 AAA 97
QY 2677 AAA 2679
DB 96 AAA 94

Search completed: January 15, 2005, 06:44:45
Job time: 1397 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 04:02:42 ; Search time 11079 Seconds
(without alignments)
11435.067 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagaattcgcagcagcgccg.....acaaaaaaaaaaaaaaaaa 2679

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 20 *or greater*

Total number of hits satisfying chosen parameters: 72274

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hgt: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_stg: 12: gb_sy: 13: gb_un: 14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2679	100.0	2679	9 AF170724	Homo sapi
2	2133	79.6	2639	6 AX877194	Sequence
3	2133	79.6	2639	6 BD156534	Primer fo
4	2133	79.6	2639	9 AK027687	Homo sapi
5	2031	75.8	3189	9 BC012072	Homo sapi
6	1618	60.4	3181	6 AX405642	Sequence
7	1465	54.7	3138	6 AX877222	Sequence
8	1465	54.7	3138	6 BD156548	Sequence
9	1465	54.7	3138	6 AK001658	Primer fo
10	944	35.2	2448	6 AK834949	Sequence
11	944	35.2	2448	9 AK097671	Homo sapi
12	930	34.7	6235	6 BD183291	Novel gen
13	909	33.9	2257	9 AK090948	Homo sapi
14	633	23.6	2186	6 AX713476	Sequence
15	633	23.6	2186	9 AK054917	Homo sapi
16	483	18.0	1085	6 CQ719882	Sequence
17	478	17.8	816	6 AX868758	Sequence
18	478	17.8	816	6 BD148820	Primer fo
19	468	17.5	824	6 AX868776	Sequence

20	468	17.5	824	6 BD148838	Primer fo
21	426	15.9	518	6 AX873789	Sequence
22	426	15.9	518	6 BD153851	Primer fo
23	386	14.4	1810	9 AC127070	Homo sapi
24	386	14.4	181438	2 AC023047	Homo sapi
25	218	8.1	181438	2 AC023047	Homo sapi
26	98	3.7	756	11 BV180578	Sequence
27	97	3.6	601	11 BV168191	Sequence
28	78	2.9	617	6 AX385952	Sequence
29	60	2.2	60	6 CQ356585	Sequence
30	38	1.4	158897	2 AC118260	Sequence
31	37	1.4	3194	10 BC049792	Sequence
32	37	1.4	321708	2 AC087142	Sequence
33	37	1.4	338116	2 AC087159	Sequence
34	34	1.3	202792	2 AC125898	Sequence
35	32	1.2	601	11 BV002855	Sequence
36	29	1.1	124973	8 AC124951	Sequence
37	28	1.0	146516	2 AC079981	Sequence
38	28	1.0	218226	2 AC126634	Sequence
39	28	1.0	228987	2 AC111838	Sequence
40	28	1.0	274796	2 AC097665	Sequence
41	27	1.0	167166	2 AC117568	Sequence
42	27	1.0	167938	10 AC115904	Sequence
43	27	1.0	221753	10 AC140355	Sequence
44	27	1.0	230221	10 AC123851	Sequence
45	27	1.0	234393	10 AL772311	Sequence
46	27	1.0	239783	2 AC102564	Sequence
47	27	1.0	266632	2 AC129762	Sequence
48	27	1.0	269117	2 AC115400	Sequence
49	27	1.0	322833	2 AC131863	Sequence
50	26	1.0	444	8 ATMS29544	Sequence
51	26	1.0	860	6 B77096	Sequence
52	26	1.0	860	8 CACORAT16	Sequence
53	26	1.0	3144	3 AY061591	Sequence
54	26	1.0	61165	10 AL669936	Sequence
55	26	1.0	68445	2 AC025193	Sequence
56	26	1.0	94784	9 AL355309	Sequence
57	26	1.0	102008	2 AC016552	Sequence
58	26	1.0	113950	8 AC004687	Sequence
59	26	1.0	134347	9 AL356295	Sequence
60	26	1.0	149509	5 BX005028	Sequence
61	26	1.0	152968	2 AC073669	Sequence
62	26	1.0	155451	2 BX942846	Sequence
63	26	1.0	157262	10 AC121945	Sequence
64	26	1.0	168473	5 BX649544	Sequence
65	26	1.0	176196	5 AL928676	Sequence
66	26	1.0	179683	2 AC115823	Sequence
67	26	1.0	182082	2 AC092842	Sequence
68	26	1.0	185951	2 AC024386	Sequence
69	26	1.0	198939	2 BX957279	Sequence
70	26	1.0	201467	9 AC093690	Sequence
71	26	1.0	201949	2 AC109165	Sequence
72	26	1.0	205547	10 AC073938	Sequence
73	26	1.0	222149	2 AC115978	Sequence
74	26	1.0	222932	2 AC137869	Sequence
75	26	1.0	231676	2 AC117155	Sequence
76	26	1.0	231895	2 AC127043	Sequence
77	26	1.0	232876	10 AC140338	Sequence
78	26	1.0	236350	10 AC020971	Sequence
79	26	1.0	239859	2 AC119482	Sequence
80	26	1.0	241112	2 AC106261	Sequence
81	26	1.0	245325	9 AC008499	Sequence
82	26	1.0	257666	2 AC121225	Sequence
83	26	1.0	268208	2 AC106229	Sequence
84	26	1.0	286524	2 AC106223	Sequence
85	25	0.9	442	8 ATMS29842	Sequence
86	25	0.9	468	5 BC053809	Sequence
87	25	0.9	870	8 AP425601	Sequence
88	25	0.9	1085	6 AR321631	Sequence
89	25	0.9	1400	3 AY069274	Sequence
90	25	0.9	1468	10 BC025901	Sequence
91	25	0.9	1583	9 AB048887	Sequence
92	25	0.9	1963	6 AX406978	Sequence

c 969	23	0.9	212049	5	EX005484	EX005484 Zebrafish
970	23	0.9	213473	10	AC134869	AC134869 Mus muscu
971	23	0.9	213580	2	AC109224	AC109224 Mus muscu
c 972	23	0.9	213817	2	AC051615	AC051615 Mus muscu
973	23	0.9	213884	2	AC147475	AC147475 Mus muscu
c 974	23	0.9	213933	2	AC128930	AC128930 Rattus no
975	23	0.9	214438	10	AC124546	AC124546 Mus muscu
c 976	23	0.9	215019	10	AC107703	AC107703 Mus muscu
c 977	23	0.9	215571	10	AC116115	AC116115 Mus muscu
978	23	0.9	216172	9	AC148958	AC148958 Ocolemur
c 979	23	0.9	216172	9	AC098973	AC098973 Homo sapi
c 980	23	0.9	216444	2	AC116858	AC116858 Mus muscu
c 981	23	0.9	216501	10	AC107795	AC107795 Mus muscu
c 982	23	0.9	216502	2	AC109509	AC109509 Mus muscu
983	23	0.9	216567	2	CR558305	CR558305 Danio rer
c 984	23	0.9	216885	2	CR582328	CR582328 Mus muscu
985	23	0.9	218074	2	AC103155	AC103155 Rattus no
c 986	23	0.9	218283	10	AC132382	AC132382 Mus muscu
c 987	23	0.9	218688	10	AC132452	AC132452 Mus muscu
988	23	0.9	220193	10	AC131713	AC131713 Mus muscu
989	23	0.9	220454	2	CR382335	CR382335 Danio rer
c 990	23	0.9	220558	2	CR522881	CR522881 Danio rer
c 991	23	0.9	220874	2	CR376848	CR376848 Danio rer
992	23	0.9	221190	2	EX571704	EX571704 Danio rer
c 993	23	0.9	221405	2	AC114252	AC114252 Rattus no
c 994	23	0.9	221649	2	AC131083	AC131083 Mus muscu
995	23	0.9	222291	2	AC020860	AC020860 Mus muscu
c 996	23	0.9	222314	2	AC112362	AC112362 Rattus no
c 997	23	0.9	222358	2	AC099385	AC099385 Rattus no
998	23	0.9	222370	2	AC105895	AC105895 Rattus no
999	23	0.9	222805	2	AC133501	AC133501 Mus muscu
c1000	23	0.9	223443	2	AC112801	AC112801 Rattus no

ALIGNMENTS

RESULT 1	AF170724	2679 bp	mRNA	linear	PRI 03-AUG-2000
LOCUS	AF170724				
DEFINITION	Homo sapiens cell cycle checkpoint protein CHFR mRNA, complete cds.				
ACCESSION	AF170724				
VERSION	AF170724.1	GI:9651169			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	Scolnick,D.M. and Halazonetis,T.D.				
AUTHORS	Scolnick,D.M. and Halazonetis,T.D.				
TITLE	Chfr defines a mitotic stress checkpoint that delays entry into metaphase				
JOURNAL	Nature 406 (6794), 430-435 (2000)				
MEDLINE	20388685				
PubMed	10935642				
REFERENCE	2 (bases 1 to 2679)				
AUTHORS	Halazonetis,T.D. and Scolnick,D.M.				
TITLE	Direct Submision				
JOURNAL	Submitted (21-JUL-1999) Wistar Institute, 3601 Spruce Street, Philadelphia, PA 19104, USA				
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ORIGIN

Query Match	100.0%	Score 2679;	DB 9;	Length 2679;
Best Local Similarity	100.0%	Pred. No. 0;		
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			Indels	0;
			Gaps	0;
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1	AMGAATTCGGGACGACGCGCGCAATCTCTTGACAGCGCGCGCGCGCGCGGTTCCGG	60		
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61	GTTTCGGCGCGCGCGCGGATGTGAATCCGATGAGCGCGCGCGCGCGCGGATGCG	120		
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121	CGCGCGCGCGCGCGCGGATGTGAATCCGATGAGCGCGCGCGCGCGGATGCG	180		
181	GTCCTCTGAGGAGCGCGGATGTGAATCCGATGAGCGCGCGCGCGCGGATGCG	240		
181	GTCCTCTGAGGAGCGCGGATGTGAATCCGATGAGCGCGCGCGCGGATGCG	240		
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241	CCGACCAATTAACCTGCTCTGAGATCATCTGATGATGATGATGATGATGATGATGAT	300		
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301	CAGGTGACATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360		
361	AAGAAGACATGCGCTCTGAGATCATCTGATGATGATGATGATGATGATGATGAT	420		
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481	CAAGATCTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540		
481	CAAGATCTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540		
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841	GAGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900		

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841 GAGATTTTGAAGCCGCTGAAGAAATGAGAGATGGAGACCTTGAACCTGAACGCG 900
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Db 901 CAGTTTGTGGTCCGACAAACCGCTAGAAATGCCAAACCGTCCAGAGAGCTCAAGCA 960
QY 961 GCGGCTGGGAAAGCCAGCAAGATGAGAGAGCGCTGACATGATCATCTGCCAGAGCTTG 1020
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Db 1321 CTGTGAGAGTGAAGTGAAGTCTGACATTAAGCAGCAGATGATGATGATGATGATG 1380
QY 1381 TGTCTGAGTGAAG 1440
Db 1381 TGTCTGAGTGAAG 1440
QY 1441 CAG 1500
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Db 1801 TGGAAAAACATGTTGACCGAGAGCTGCTGCTTCCAGCGGAGAGTGTCTGCTGCT 1860
QY 1861 GATTACAGAGTCAAG 1920
Db 1861 GATTACAGAGTCAAG 1920
QY 1921 GAGCTGACCTATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GAGCTGACCTATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980

Db 1921 GAGCTGACCTATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 TCCCGTCTGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 TCCCGTCTGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
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Db 2101 GAGAGCTTTTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
QY 2161 TGAAGGTGTTTCAAG 2220
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QY 2221 GGTGACTCTTCTGAG 2280
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QY 2641 ATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2679
Db 2641 ATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2679

RESULT 2
AX877194 2639 bp DNA linear PAR 17-DEC-2003
LOCUS AX877194
DEFINITION Sequence 12099 from Patent EP1074617.
ACCESSION AX877194
VERSION AX877194.1 GI:40031930
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Ota, T., Iwagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primers for synthesizing full-length cDNA and their use
Patent: BP 1074617-A 12099 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JBP)
FEATURES
source location/Qualifiers
1..2639
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/mol_type="unassigned DNA"
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CDS

79..2037
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ORIGIN

Query Match 79.6%; Score 2133; DB 6; Length 2639;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 GATACCTCAGGTGACAGGTGACAGGCGAGGCGGATCCCGGGGATCCCGTCCGTGCGCC 588
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QY 589 GCCACTCAGGTGTGCTTTGAGGAAACCAAGCCATCAACATCGACGTCAAGACTCTTCCCC 648
DB 541 GCCACTCAGGTGTGCTTTGAGGAAACCAAGCCATCAACATCGACGTCAAGACTCTTCCCC 600
QY 649 AAGAGCTCGGCTCTTCCACGAGGCTTCTCTGCAAGGCGAGAGCGTTCCTCCAGTTGT 708
DB 601 AAGAGCTCGGCTCTTCCACGAGGCTTCTCTGCAAGGCGAGAGCGTTCCTCCAGTTGT 660
QY 709 GGGTCTGGGGGTGTGTGACATCTCCCTAAAGAAAGTGTCTCTGTGGCAAGTATGA 768
DB 661 GGGTCTGGGGGTGTGTGACATCTCCCTAAAGAAAGTGTCTCTGTGGCAAGTATGA 720
QY 769 GTTCCAGCTTTGCTCAGCTCTCCACAGAAAGACTGCGTCTTTTGTGTGAA 828
DB 721 GTTCCAGCTTTGCTCAGCTCTCCACAGAAAGACTGCGTCTTTTGTGTGAA 780
QY 829 CCCGAGATCAGAGAGATTTGAGGCCCTGAGAAAGAAATGAGAGAGATGAGGACCTT 888
DB 781 CCCGAGATCAGAGAGATTTGAGGCCCTGAGAAAGAAATGAGAGAGATGAGGACCTT 840
QY 889 GACCTGAAACGGGCAATTTGTGTGACCAACCGCGTAAAGAAATGCCCAACCGTCCACGAG 948
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QY 1009 TGCCAGAGCCTGCTCAAGACCTGCGTAGTTTGACGCCCTGATCAACAGTTTGGCCCG 1068
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QY 1849 TTTCTGTGTCTGATTAACAGAGTCAAGGAGACACCGTTCTGTGTAACTGCTGTGCGCTG 1908
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QY 1909 GCGAGCTTCGCTGAGCTGACCTATCAGTATCGGAGAACATTCGCTTCCGAGTGTGCA 1968
DB 1861 GCGAGCTTCGCTGAGCTGACCTATCAGTATCGGAGAACATTCGCTTCCGAGTGTGCA 1920
QY 1969 GTGCGCGTGAATCCGCTCTGACTGCTGCTGAGGAGGCTGACCTCCGACTCAGGTGAA 2028
DB 1921 GTGCGCGTGAATCCGCTCTGACTGCTGCTGAGGAGGCTGACCTCCGACTCAGGTGAA 1980
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DB 2041 TCCAGAGGCGCTGAGAGCTTTGACACTGAGAGTGAAGAGGCTGTTTAAATATCA 2100
QY 2149 GAGCAAGACAGTCAAGTGTGTTTCAAGCCCTTGAAGGAGAGGAGGAGTCTCCGA 2208
DB 2101 GAGCAAGACAGTCAAGTGTGTTTCAAGCCCTTGAAGGAGAGGAGGAGTCTCCGA 2160
QY 2209 CAGGTGCTGTGGGTGACTCTTCTGTGAGAGCTTTTAAACCTGTGAGTGAAGCTTCCCA 2268
DB 2161 CAGGTGCTGTGGGTGACTCTTCTGTGAGAGCTTTTAAACCTGTGAGTGAAGCTTCCCA 2220
QY 2269 GAGCGCGGAGGAGCGAGCGCGCTCTGAGAGAGCTGAGGAGCTGAGTGTGAGCAT 2328
DB 2221 GAGCGCGGAGGAGCGAGCGCGCTCTGAGAGAGCTGAGGAGCTGAGTGTGAGCAT 2280
QY 2329 CAGCAGAGAGACAGAGCTTTTGTGAACATGCGGCGCTCCCGCGAGAGGAGGAGTGT 2388
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Db	2401	TCAAGGAGAAAGGCGCAGTTTATCAAAAACATTTGTTTCAGGAGAAAGGAGCATTAAGTTTA	2460
Qy	2509	CAGCCTAAGAACCGTACACAATATCTCTCTCTGTGGGAAAACACACAGCATTTTATCTATT	2568
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Qy	2569	TTTATTTTAAATAGGTTTGTCCTTATCTCTTAATAGATTTTAAATGTCAACAACTGTAGC	2628
Db	2521	TTTATTTTAAATAGGTTTGTCCTTATCTCTTAATAGATTTTAAATGTCAACAACTGTAGC	2580
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RESULT 3	BD156534	2639 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD156534				
DEFINITION	Primer for synthesizing	full-length cDNA	and use thereof.		
ACCESSION	BD156534				
VERSION	BD156534.1	GI:27862292			
KEYWORDS	JP 20020191363-A/11377.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 2639)
Otsu,T., Itoogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ichi,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11377 09-JUL-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/11377
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12O1/68//C12P21/08 G06F17/30 C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
(79) . . (2034) .
FT CDS

FEATURES	Location/Qualifiers
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ORIGIN

Query Match	79.6%	Score 2133	DB 6	Length 2639
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2133; Conservative	0	Mismatches	0	Gaps 0

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Db	541	GCACCTCAGTGTGATTGAGGAAACACAGCCATCAATCAGCTCAGACTCTTCTCC	600

QY	649	CAAGCTCGGCTCTTTCACAGGAGCCCTTCTCAGAGGCGAGGCGTTCTCCAGTTG	708
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QY	709	GGGCTCGGAGGTGTGTCATCTCCCTTAAGAGAGTGGTCCCTCTGTCGCAAGTATGA	768
Db	661	GGGCTCGGAGGTGTGTCATCTCCCTTAAGAGAGTGGTCCCTCTGTCGCAAGTATGA	720
QY	769	GTCTCCAGCTTTGCTTCAAGCTCTCCAGACAGAAAGACTGCTCTTTTCGTGTGAA	828
Db	721	GTCTCCAGCTTTGCTTCAAGCTCTCCAGACAGAAAGACTGCTCTTTTCGTGTGAA	780
QY	829	CCCCAGAGTACAGAGATTTGGACCCCGTGAAGAAATGAGAGAGANTGGGACCTT	888
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QY	889	GACCTGAACGGGCGATTGTTGGTGGCAACAACGGGTGAATATGGCCAAACGTCCACGAG	948
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QY	1249	CAAGCAATGCTGACGCCCAAGATGACAGGCGGCTTTTCTGATGAAGAAAGGAGTTCAAG	1308
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Db	1621	ACCGGCTCTACAGGCTGCTGGCCCGCTTTGTAGCTCAACCTGGGTGACAAATGTCTG	1680
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Db      1801 TTTTCTCTGTCTGATTATTCAGAGTCAAGGAGACACCGTTCTGTGTTACTGCTGTGCTTG 1860
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ORGANISM

REFERENCE

AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1

TITLE

Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

REFERENCE

AUTHORS

Isoigai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Aotsuka, S., Yoshikawa, Y.,
Matsunawa, H., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,
Makamatsu, A., Nakamura, Y., Nagahara, K., Masuno, Y., and Sasaki, N.

NEBO human cDNA sequencing project

TITLE

AUTHORS

Unpublished
3 (bases 1 to 2639)
Isoigai, T. and Otsuki, T.
Direct Submission

COMMENT

Submitted (10-MAY-2001) Takao Isoigai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5' & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES

SOURCE

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induction."
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/note="unlabeled protein product"
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CDS

RESULT 4
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DEFINITION to TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.
ACCESSION AK027687
VERSION AK027687.1 GI:14042552
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)

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DEFINITION Sequence 57 from Patent W00222660.
ACCESSION AX405642
VERSION AX405642.1 GI:21438723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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QY	2449	TCAAAGGAGAAAGGCAAGTTTATCAAAAACATTTGTTTCAGAGAAAGGAGCATAGTTTA	2508
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VERSION	AX877222.1 GI:40031958	

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REFERENCE
AUTHORS Ota, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsubuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 12127 07-FEB-2001; Research Association for Biotechnology (JP)

FEATURES	RESEARCH ASSOCIATION FOR BIOCHEMISTRY (OF
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Qy	GTCTTCACACTTtGCTCTGAGCTTCTCCCAACACAGAAAGACtTGCTCTTTCTGTGTGGAA	828
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QY	889	GACCTGAACGGGCAAGTTGTTGGTGGCAACACCGGCTAGAAATGGCCAAACCGTCAAGAG	948
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Db	1520	ACCGGCTGCTACGGCTGCTGGCCCGCTTTTGTAGCTCAACCTGGGTGACAAAGTGTCTG	1579
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QY	2089	TCGAGAGCGCCTGAGCAGCTTTACGACACTGAGGTGAAGAGACGTGTTTTAAATCA	2148
Db	1940	TCGAGAGCGCCTGAGCAGCTTTACGACACTGAGGTGAAGAGACGTGTTTTAAATCA	1999
QY	2149	GAGAACAGCAGCTCAAGGTGTTTTACAGCCCCCTGAGGAAAGGAGCGCAGGTCTCCGA	2208
Db	2000	GAGGCAAGCAGCTCAAGGTGTTTTACAGCCCCCTGAGGAAAGGAGCGCAGGTCTCCGA	2059
QY	2209	CAGGTGCTCTGGGGTGACTCTTCTCTGTGAGCTTTTACCCCTGAGTGAACCCCTCCCA	2268
Db	2060	CAGGTGCTCTGGGGTGACTCTTCTCTGTGAGG - TTTAACCTCTGAGTGAACCCCTCCCA	2117
QY	2269	GAGCCCCGGGGGCGCCAGCCCGCCTCTCTGTGAGCGCTGGCAGGCGCTCGTGGGCAT	2328
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QY	2329	CAGCAGCAGACAGCAAGCCTTCTGTACATGCGGCGCTGCCGCGAGAGGGGAGCTTT	2388
Db	2178	CAGCAGCAGACAGCAAGCCTTCTGTACATGCGGCGCTGCCGCGAGAGGGGAGCTTT	2237
QY	2389	GCTCTTTTGTACATTTTCCGAAACTACAGTTAAGCAGAGAAGCTGTGTTACAGAAAAGTT	2448
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QY	2509	CAGCCTACAGACGTAACAATATCTCTGCTGCTGGGAAACACACAGATTTTATCTATTT	2568
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LOCUS	BD156548	Primer for synthesizing full-length cDNA and use thereof.	
DEFINITION	BD156548		
ACCESSION	BD156548.1	GI:27862306	
VERSION	BD156548.1	GI:27862306	
KEYWORDS	JP 2002191363-A/11391.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Ota,T., Iwagui,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,U., Iehi,S., Sugiyama,T., Wakematsu,A., Nagai,K. and Otsuki,T.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 11391 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE		
	OS Homo sapiens (human)		
	PN JP 2002191363-A/11391		
	PD 09-JUL-2002		
	PF 28-JUL-2000 JP 2000280990		

	PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KIORU
	PI	SATRO.
	PI	DUNICHI YANAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU
	PI	KEIICHI NAGAI, TETSUJI OTSUKI
	PC	
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QY	889	GACCTGAAACGGGACGATTGGTGTGGCAACACCGGTAGAAATGGCCAAACCGTCCAGAG 948
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Db	1100	CAAGACATGCTGACGCCCAAGGTACAGCGCGCTCTTTTCTGATGAAGAGGAGATTCAAG 1159
QY	1309	GACCTGCTGGAGCGTGTAGACGTTGACAGTAGAGTCTCAGACATTAGCAGCCATPACGTC 1366
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QY	1429	CCCCAGGGCCGACCCAGAGGCCCCCAAGGCGCTGGGGGATGACCTCTCAAGTCCGTCAAGC 1488
Db	1280	CCCCAGGGCCGACCCAGAGGCCCCCAAGGCGCTGGGGGATGACCTCTCAAGTCCGTCAAGC 1339

OY	1489	TTGACGACGAGAGTCCAGATTAACGTGAGCCCTCTGCAAGGAAGCAAGCCCTGTGACAC	1548
Db	1340	CTGACGACGACGAGTCCAGATTTACGTGTGCCCTCTGCAAGGAAGCAAGCCCTGTGACAC	1399
OY	1549	TGCTGCTTCCAGCCCATCCGACCCGAGAGCGAGCGGACGACGACCCGCGTGTGCC	1608
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OY	1609	CCTCAGCAGTGTGCGGTCTGCTGTGAGCCTTTCTGCCACCTGTACTGGGGCTTGACCCCGG	1668
Db	1460	CCTCAGCAGTGTGCGGTCTGCTGTGAGCCTTTCTGCCACCTGTACTGGGGCTTGACCCCGG	1519
OY	1669	ACCGGCTGCTACGCGTGCCTGGCCCCCGTTTGTGTGAGCTCAACTGTGGGTGACAGTGTCTG	1728
Db	1520	ACCGGCTGCTACGCGTGCCTGGCCCCCGTTTGTGTGAGCTCAACTGTGGGTGACAGTGTCTG	1579
OY	1729	GACGCGGTGTGACACACACACAGCTTACAGTACACATCTGTGAAGATTACCTGTGCAACC	1788
Db	1580	GACGCGGTGTGACACACACAGCTTACAGTACACATCTGTGAAGATTACCTGTGCAACC	1639
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OY	1849	TTTCTGCTGTCTGATTACAGAGTCAAGGAGACACCCGTTCTGTGTTACTGTGTGTGCCCTG	1908
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OY	1909	CGCAGCTTCCGTGAGCTGACCTTATCAGTATGGGAGAACATTCCTGCTTCCGAGTGTGCA	1968
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OY	1969	GTGGCGGTAAACATCCCGTCTGTGACTGTGAGCGGCGGTAACTGCGCAGCTCAGGTGAAA	2028
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OY	2089	TCCAGAGGCCCCGACACAGTTTACACACTGGAGGTGAAGAGCGGTGTTTTTAAATPACA	2148
Db	1940	TCCAGAGGCCCCGACACAGTTTACACACTGGAGGTGAAGAGCGGTGTTTTTAAATPACA	1999
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Db	2000	GAGGCAACACGTCAAAGGTGTTTTACAGCCCCCTGAGGAGAAAGGACGACAGGCTCCGCA	2059
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OY	2389	GCTCTTTGTATCTTTCCGAAACTACAGTTTAAACGGAAAGTCTGTTTTCAGGAAATTT	2448
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OY	2509	CAGCCTTACAGACGTACACAAATATCTGTGTGTGGGAAAAACACAGCATTTTATCTATTT	2568
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[illegible]

etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 54.7%; Score 1455; DB 9; Length 3138;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY	709	GGGTCGGGGGTGGTGGCATCTCCCTAAAGAAAGTGTCCCTGTGGCAAGTATGAA	768
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DB	1400	TGCTGCTTCCAGCCCATGCCCCGACCGAGAGCGAGCGCAGACAGAACCCGCTGTGCGC	1459
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QY	1969	GTGGCGTGAATCCCGTCTGACGTGCTAAGGGGCGTAACTGCGCAGCTCAGGTGAA	2028
DB	1820	GTGGCGTGAATCCCGTCTGACGTGCTAAGGGGCGTAACTGCGCAGCTCAGGTGAA	1879
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Negahari, K. and Masuho, Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1347046-A 2073-24-SEP-2003;
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ORIGIN

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 Db 1017 CGTGTGCGGAGAGTGTCTGAGTGAAG 1076
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 Db 1077 ACCCGAGGCGAGAGCCAG 1136
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 Db 1257 CCTGACAGAGTGTGCGGTGCTGCTGAG 1316
 QY 1668 GACCGGCTGCTACGGCTGCTGCTGCGCCCGCTTTTGTG 1702
 Db 1317 GACCGGCTGCTACGGCTGCTGCTGCGCCCGCTTTTGTG 1351

RESULT 11
 AK097671 2448 bp mRNA linear PRI 30-JAN-2004
 LOCUS AK097671
 DEFINITION Homo sapiens cDNA FLJ40352 fls, clone TBS2103505, highly similar to Homo sapiens cell cycle checkpoint protein CHFR mRNA.
 ACCESSION AK097671
 VERSION AK097671.1 GI:21757518
 KEYWORDS Oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Odayaashi, M., Nishii, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J. I., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosotani, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, F., Furuya, T., Kikukawa, M., Oimura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Niinomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimura, M., Watanabe, M., Hirooka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S.,

Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shibata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Tereshima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mitoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabara, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Saitoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Maehuo, Y., Yamauchi, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

14702039

2

Oshima, A., Takahashi, Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Magaki, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, T., Sugano, S., Nagahori, K., Maehuo, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 2448)

Isogai, T. and Yamamoto, J.

Direct Submision

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan Reconstruction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

1..2448

source

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TBST12033505"

/issue_type="testis"

/clone_id="TBST12"

/note="Cloning vector: pME18SFL3"

ORIGIN

Query Match 35.2%; Score 944; DB 9; Length 2448;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 708 TGGGCTGGGGGTGGGATCTCCCTAAAGAGAGTGTCCCTGTGGCAAGTGATGA 767

DB 357 TGGGCTGGGGGTGGGATCTCCCTAAAGAGAGTGTCCCTGTGGCAAGTGATGA 416

QY 768 AGTCTCCAGCTTGGCTGAGCTCTCCCAACAGAAAGATGGCTCTTTTCTGCTTGA 827

DB 417 AGTCTCCAGCTTGGCTGAGCTCTCCCAACAGAAAGATGGCTCTTTTCTGCTTGA 476

QY 828 ACCCCGAGATCGAGAGATTGGAGCCCGGAAAGAAATGAGAGAGATGGGAGCT 887

DB 477 ACCCCGAGATCGAGAGATTGGAGCCCGGAAAGAAATGAGAGAGATGGGAGCT 536

QY 888 TGACCTGAACGGGACGATTGTTGGTGCACAAACCGGTGAATGCCAAACCGTCCACGA 947

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QY 948 GGAAGCTGAGACGAGGGCTGGGAAAGCCAGACAAAGTGAAGAGAGCGTGAATGATCAT 1007

DB 597 GGAAGCTGAGACGAGGGCTGGGAAAGCCAGACAAAGTGAAGAGAGCGTGAATGATCAT 656

QY 1008 CTGCCAGAGACCTGTGCACGACTGGCTGAGTTTGGAGCCCTGCATGACACAGTTTGGGC 1067

DB 657 CTGCCAGAGACCTGTGCACGACTGGCTGAGTTTGGAGCCCTGCATGACACAGTTTGGGC 716

QY 1068 GCGTTGCTACTCGGAGTGAATGAGAGCGCTCGTCTGTGCTTACTCTCGCGTCCGT 1127

DB 717 GCGTTGCTACTCGGAGTGAATGAGAGCGCTCGTCTGTGCTTACTCTCGCGTCCGT 776

QY 1128 GGAGCGATCTGTAAAAACCATCTCCAAACAACTCGTGAAGAGATCTCATCGACA 1187

DB 777 GGAGCGATCTGTAAAAACCATCTCCAAACAACTCGTGAAGAGATCTCATCGACA 836

QY 1188 TCACAGACAAAGTGCAGTGAAGAAAGATGCAAGATGCAAGATGCAAGATTAATAC 1247

DB 837 TCACAGACAAAGTGCAGTGAAGAAAGATGCAAGATGCAAGATGCAAGATTAATAC 896

QY 1248 TCACAGACATGCTGCAGCCCAAGTCAAGCGGCTTTTCTGTATGAAGAGAGTTTCA 1307

DB 897 TCACAGACATGCTGCAGCCCAAGTCAAGCGGCTTTTCTGTATGAAGAGAGTTTCA 956

QY 1308 GGAAGCTGCTGAAGCTGTGACAGTGAAGTGCATGAGATTCATGACGACCATAGCT 1367

DB 957 GGAAGCTGCTGAAGCTGTGACAGTGAAGTGCATGAGATTCATGACGACCATAGCT 1016

QY 1368 CGTGTCCCGGAGAGTCTCTGAGTACAGAAAGGAGCGGCGAGCTCCCACTGCCAC 1427

DB 1017 CGTGTCCCGGAGAGTCTCTGAGTACAGAAAGGAGCGGCGAGCTCCCACTGCCAC 1076

QY 1428 ACCCGAGGCGAGACCGAGAGCCCAAGGAGCGGCGGATGACACCTTCACGTCGTG 1487

DB 1077 ACCCGAGGCGAGACCGAGAGCCCAAGGAGCGGCGGATGACACCTTCACGTCGTG 1136

QY 1488 CCTGACGACGAGTCCAGGATTAAGTGTGCTCTGCAAGGAGACGCGCTGTGAC 1547

DB 1137 CCTGACGACGAGTCCAGGATTAAGTGTGCTCTGCAAGGAGACGCGCTGTGAC 1196

QY 1548 CTGCTGCTTCCAGCCCATGCCCAGCCGAGAGCGGAGCGGAGCAGACCCGCTGTG 1607

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QY 1608 CCTTGAAGAGTGTGCGGTCTGCTGACGCTTTCTGCCACCTGTATCTGGGGCTGACCCG 1667

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QY 1668 GACCGGCTGCTACGAGCTGCGTGGCCCGGTTTGTG 1702

DB 1317 GACCGGCTGCTACGAGCTGCGTGGCCCGGTTTGTG 1351

RESULT 12

BD183291 6235 bp DNA linear PAT 17-JUN-2003

LOCUS BD183291

DEFINITION Novel genes and proteins encoded by the genes.

ACCESSION BD183291.1 GI:31875491

VERSION BD183291.1

KEYWORDS JP 2002345492-A/4.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 6235)

AUTHORS Ohara, O., Nagase, T. and Nakajima, D.

TITLE Novel genes and proteins encoded by the genes

JOURNAL Patent: JP 2002345492-A 4 03-DEC-2002;

KAZUSA DNA RESEARCH INSTITUTE
OS Homo sapiens (human)

FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA"
ORIGIN	/db_xref="taxon:9606"

ORIGIN

Query Match	34.7%;	Score 930;	DB 6;	Length 6235;
Best Local Similarity	99.7%;	Pred. No. 0;		

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Db	4447	CAGTTCAGAGATTACGTGTGCCCTCTGCAAGAAAGCAGCCCTGTGTACCTGTCTCTCC	4500
OY	1559	AGCCCATGCCGACCGGAGAGCGGACGAGCAGACGACCCTGCTGTGCCCTCAGCAGT	1618
Db	4507	AGCCCATGCCGACCGGAGAGCGGAGCGGACGAGACCGCGGTGTCTGCCCTCAGCAGT	4566
OY	1619	GTGCGGTCTGCTGTGAGCCTTTCTGTGCACCTGTACTGTGGGCTGTACCCGGACCGGTGT	1677
Db	4567	GTGCGGTCTGCTGTGAGCCTTTCTGTGCACCTGTACTGTGGGCTGTACCCGGACCGGTGT	4622
OY	1679	ACGGGTGCTGGCCCCGGTTTGTGAGCTCAACCTGGGTGACAAAGTGTCTGTGACCGCGTGC	1733
Db	4627	ACGGGTGCTGGCCCCGGTTTGTGAGCTCAACCTGGGTGACAAAGTGTCTGTGACCGCGTGC	4688
OY	1739	TGAACAAACAAGCTTACGAGTGTGACATCTGTGAATAATTACTGTGCAACAGAGGTTTGA	1798
Db	4687	TGAACAAACAAGCTTACGAGTGTGACATCTGTGAATAATTACTGTGCAACAGAGGTTTGA	4744
OY	1799	CATGGAATAACATGTTGACCGAGAGCTTGTGGCTCTCCAGCGGGAAGTGTTCGTGT	1855
Db	4747	CATGGAATAACATGTTGACCGAGAGCTTGTGGCTCTCCAGCGGGAAGTGTTCGTGT	4800
OY	1859	CTGATTACAGAGTCAACGGGAGACACCGTTCTGTGTTACTGTCTGTGTGCTGTGCGCAGCTTC	1912
Db	4807	CTGATTACAGAGTCAACGGGAGACACCGTTCTGTGTTACTGTCTGTGTGCTGTGCGCAGCTTC	4866
OY	1919	GTGAGCTGACCTATCAGTATCGGGAGAAACATTCCGTTCGAGTTGCAGTGTGCGGCGTTA	1976
Db	4867	GTGAGCTGACCTATCAGTATCGGGAGAAACATTCCGTTCGAGTTGCAGTGTGCGGCGTTA	4922
OY	1979	CATCCCGTCTGTACTGTCTATCTGGGCGCGTAACTGTCCGCACTCAAGGTGAAGCTCAACG	2038
Db	4927	CATCCCGTCTGTACTGTCTATCTGGGCGCGTAACTGTCCGCACTCAAGGTGAAGCTCAACG	4988
OY	2039	CCATGAATTCATATATATCTGTGAACAGACAAGTTCAAAAATTAGATCTCAAGAGGCC	2099
Db	4987	CCATGAATTCATATATATCTGTGAACAGACAAGTTCAAAAATTAGATCTCAAGAGGCC	5046
OY	2099	CTGAGCAGCTTCAACACTGTGAGGTGAAGAAGCGTTTTTAAATACAGAGCAAGCA	2155
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OY	2159	CGTCAAGGTGTTTCAACAGCCCTGTGAGGAAAGGACGAGGGTCTCCGACAGGTGCTCT	2218
Db	5107	CGTCAAGGTGTTTCAACAGCCCTGTGAGGAAAGGACGAGGGTCTCCGACAGGTGCTCT	5166
OY	2219	GGGGTGACTCTTCTGTGAGCTTTTAACTCTGAGTGAACCTTCCCAAGGCCCGGG	2276

Db	5167	GGGGTGACCTTTCGTGTGAGAC--TTTACCGCTGAGTGAGACCCCTCCCGAGAGCCCGGG	5224
QY	2279	GGCGCGAGCCCGCCCTCTCTG3GTGA6CGCGCTG3G3CAAGG3CTG7GTGGCATCAGCAGAGA	2338
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QY	2339	GACGAGCCCTTTCTGTATACATGCGGCGCTCCCGCCGAGAGGGGCGAGTTTGTCTTTTGT	2398
Db	5285	GACGAGCCCTTTCTGTATACATGCGGCGCTCCCGCCGAGAGGGGCGAGTTTGTCTTTTGT	5344
QY	2399	ACATTTTCCGAAACTACAGTTAAAGCAGAAAGTCTGTTTTCAGGAAAAGTTTCAAGGAGAGA	2458
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	RESULT 13
LOCUS	AK090948
DEFINITION	AK090948
ACCESSION	AK090948
VERSION	AK090948.1 GI:21749208
KEYWORDS	cilgo capping; fis (full insert sequence).
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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	Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
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	Oyama,M., Heta,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
	Saton,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
	Nagaee,T., Nomura,N., Kikuchi,H., Masuno,Y., Yamashta,R.,
	Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Nishimura, K., Matsushima, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Ito, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuko, Y., Nagai, K. and Isogai, T.

TITLE Unpublished
JOURNAL NEDD human cDNA sequencing project
REFERENCE 3 (bases 1 to 2257)
AUTHORS Isogai, T. and Yamamoto, J.
TITLES Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kametani, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDD human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES
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/note="Cloning vector: pME18SFL3"

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Matches 959; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1762 GACATCTGAAGATTACTGGCAACCAAGGTTTGAACATGAAAAACATGTTGACCGAG 1821
DB 729 GACATCTGAAGATTACTGGCAACCAAGGTTTGAACATGAAAAACATGTTGACCGAG 788
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DB 789 AGCTCTGTGGCTCTCCAGCGGGAGTGTCTGCTGTCTGATTACAGAGTCAAGGAGAC 848
QY 1882 ACCGTTCTGTGTTACTGCTGTGGCTGCGACGCTTCCGTGAGCTGACCTATCAATGATCGG 1941
DB 849 ACCGTTCTGTGTTACTGCTGTGGCTGCGACGCTTCCGTGAGCTGACCTATCAATGATCGG 908
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DB 909 CAGAACATCTCGCTTCCGAGTTGCGACAGGCGCGTAAACATCCCGTCCGACCTGACCTGAC 968
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DB 969 GGCCTGTAAGTCCGACCTCAGGTGAAGCTCACACGACCTGAATTCATATCATATCTGT 1028
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QY 2122 GTGAAGAGAGCTGTTTAAATACAGACAGACAGCTCAAGTGTTCACAGCCCC 2181
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DB 1149 CTGAGGAAAGGAGCAGAGGCTCCGACAGGAGTCTGAGGAGTCTTCTGTGAGGCT 1208
QY 2242 TTACCTCTGAGTGAACCTCCCGACAGGCCCGGGGCGCAGCCCTCTGAGTG 2301
DB 1209 TTACCTCTGAGTGAACCTCCCGACAGGCCCGGGGCGCAGCCCTCTGAGTG 1268
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QY 2362 GGCCTCCCGCAGAGAGGAGGAGTGTGCTGTTGTCATTTCCGAAACATGACGTTA 2421
DB 1329 GGCCTCCCGCAGAGAGGAGGAGTGTGCTGTTGTCATTTCCGAAACATGACGTTA 1388
QY 2422 AGCAGAGTCTGTTTCAAGAAAAGTTTCAAGGAGAGGAGGCAAGTTATCAAAAACAT 2481
DB 1389 AGCAGAGTCTGTTTCAAGAAAAGTTTCAAGGAGAGGAGGCAAGTTATCAAAAACAT 1448
QY 2482 GTTTCAGAGAAAGGAGAGTAAAGTTTACAGCTTACAGAGCTACCAATATCTCTCT 2541
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DB 1509 GGGAAACACAGAGCTTATATCTATTTTATTTTATAGGTTGGTCTTATCTTCA 1568
QY 2602 TAAGTTTAAATGTCACAACTGACAGCAAAATATATTAATTAATTAATTAATTAAT 2661
DB 1569 TAAGTTTAAATGTCACAACTGACAGCAAAATATATTAATTAATTAATTAATTAAT 1628

RESULT 14
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AX713476
LOCUS Sequence 160 from Patent EP1293569.
DEFINITION AX713476
ACCESSION AX713476
VERSION AX713476.1 GI:29888332
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Ito, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuko, Y.

TITLE Full-length cDNAs
JOURNAL Helix Research Institute (HRI); Research Association for Biotechnology (RAB)
FEATURES
source
1..2186
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 23.6%; Score 633; DB 6; Length 2186;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 863; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1796 TGACATGAAACATGTTGACGAGAGCTGCTCTTCACGCGGAGTGTTCCTGC 1855
DB 695 TGACATGAAACATGTTGACGAGAGCTGCTCTTCACGCGGAGTGTTCCTGC 754
QY 1856 TGCTGATTAACAGAGTCAAGGAGACACCGTCTGTGTGCTGTGAGCT 1915


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Db      755 TGTCTATTACAGAGTACGGGAGACACCGTTCTGTGTTTCTGCTGTGGCTCGACGACT 814
Qy      1916 TCCGTGAGTACCTCATCATGATTCGGAGAACATCTCTGCTCCAGTTGCCAGTGCCG 1975
Db      815 TCCGTGAGTACCTCATCATGATTCGGAGAACATCTCTGCTCCAGTTGCCAGTGCCG 874
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Qy      2036 ACCGCAATGAATTCATCATATCTGTGAACAACAAGTTCAAAAATAAGATCCAGAG 2095
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Qy      2156 GCACTGCAAGTGTATTCAGAGCCCTGAGGGAAGGAGCGGTCTCCAGAGTGC 2215
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Qy      2216 TCTGGGGTGACTCTTCTGTGAGCTTTTACCCTCTGAGTGAACCTCCCGACAGCC 2275
Db      1115 TCTGGGGTGACTCTTCTGTGAGC--TTTACCTCTGAGTGAACCTCCCGACAGCC 1172
Qy      2276 GGGGGCCGAGCCCGCTCTGTGTGAGCGCTGGGAGGCGCTGTGTGATCAGAGC 2335
Db      1173 GGGGGCCGAGCCCGCTCTGTGTGAGCGCTGGGAGGCGCTGTGTGATCAGAGC 1232
Qy      2336 AGAGAGCAAGCTTTCTGTGAACATGCGCGCTCCCGGAGAGGAGAGTTTGTCTTT 2395
Db      1233 AGAGAGCAAGCTTTCTGTGAACATGCGCGCTCCCGGAGAGGAGAGTTTGTCTTT 1292
Qy      2396 TGTACATTTTCCGAAATCAAGTTTAAAGAGAGTCTGTTTCAAGAAAGTTTCAAGG 2455
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Qy      2456 AGAAGGGCAAGTTTATCAAAAACATTTTCAAGAGAGGAGCATTAAGTTTACAGCT 2515
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Db      1473 TAAATAGTTTGGTCTTATCTTCTAATTAAGATTTAAATGTCACAAACTGTAGCAATA 1532
Qy      2636 ATATTAATTTAATTTAACAATTTGAC 2661
Db      1533 ATATTAATTTAATTTAACAATTTGAC 1558

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RESULT 15
LOCUS   AK054917
DEFINITION
to Homo sapiens cDNA FLJ30355 f8s, clone BRACE2007685, highly similar
to Homo sapiens cell cycle checkpoint protein CHRR mRNA.
ACCESSION
AK054917.1 GI:16549547
VERSION
AK054917.1
KEYWORDS
oligo capping; f8s (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Oka,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
Makamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,

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Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Magatsuma,M.,
Shiratori,A., Sudo,H., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
Kikkawa,B., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,
Tanikawa,M., Yamazaki,M., Nishimura,K., Ishibashi,T., Yamashita,H.,
Murakawa,K., Fujimori,K., Tanai,H., Kimura,M., Watanabe,M.,
Hirooka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,
Yosida,M., Horita,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,
Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
Takeuchi,K., Arita,M., Imose,N., Mitsuhashi,K., Yuki,H., Oshima,A.,
Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T.,
Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S.,
Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,
Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
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Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togaishi,T.,
Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Sato,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masuno,Y., Yanashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
JOURNAL
Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Makamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,K., Kanda,K.,
Magatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuno,Y., Nagai,K. and Isogai,T.
NEBD human cDNA sequencing project
Unpublished
3 (bases 1 to 2186)
REFERENCE
Isogai,T., Otsuki,T. and Sugiyama,T.
JOURNAL
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kiserazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEBD human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
HRI.
FEATURES
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/note="Cloning vector: pME18SFL3"
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Query Match 23.6%; Score 633; DB 9; Length 2186;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 863; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
Qy 1796 TGACATGAGAAACATGTTGACGAGAGCTGTGCTCTCCAGCGGGAGTGTTCCTC 1855
Db 695 TGACATGAGAAACATGTTGACGAGAGCTGTGCTCTCCAGCGGGAGTGTTCCTC 754

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 DB 815 TCCGTGAGCTGACCTTACAGTATCGGCAGAACATTCCTGCTTCGAGTTGCGAGTGGCCG 874
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 QY 1976 TAAATCCCGTCTGACTGCTGACTGCGGCGCTGAACTGCGCACTCAGGTGAAGTCACT 2035
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 DB 935 AGCCCATGAATTCATCATATCTGTGAACAGCAAGGTTCAAAACTAAGCATCCAGAG 994
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 DB 1115 TCTGAGGAGTACTCTGCTGTGAGAGCTTTTAACTGAGTGAAGCTTCCGAGAGCCG 1172
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 DB 1473 TAAATGCTTGTGCTTATCTTCTAATAAGATTAAATGTCACAACTGTAGACAAATA 1532
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RESULT 16
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 DEFINITION Sequence 5916 from Patent WO02068579.
 ACCESSION CQ719982
 VERSION CQ719982.1 GI:42280839
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kite, such as nucleic acid arrays, comprising a majority of
 humenexons or transcripts, for detecting expression and other uses
 thereof

JOURNAL Patent: WO 02068579-A 5916 06-SEP-2002;
 PE Corporation (NY). (US)
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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 Query Match 18.0%; Score 483; DB 6; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 4,1e-268;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 710 GGTCTGGGGGTGTGTGCTATCTCCCTTAAAGAGAGTGTCTCTGTGCAAGTGAAG 769
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 DB 1 GGTCTGGGGGTGTGTGCTATCTCCCTTAAAGAGAGTGTCTCTGTGCAAGTGAAG 60
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 DB 61 TCTCAGCTTTGCTCAGCTCTCCAGACAGAAAGTGTCTCTGTGTTGAAC 120
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 QY 830 CCCAGATCAGAGAGATTGAGAGCCCTGAAAGAAATGAGAGAGATGGAGACTTTG 889
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 DB 361 CTTCCTACTCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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 QY 1130 AGCGATCTGTAAACACATCTCTCAACAGCTGTGGAAGCATATCTCAGCATC 1189
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 DB 421 AGCGATCTGTAAACACATCTCTCAACAGCTGTGGAAGCATATCTCAGCATC 480
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 QY 1190 CAG 1192
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 DB 481 CAG 483
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RESULT 17
 LOCUS AX868758 816 bp DNA linear PAT 17-DEC-2003
 DEFINITION Sequence 3663 from Patent EP1074617.
 ACCESSION AX868758
 VERSION AX868758.1 GI:40023621
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Ota, T., Iwagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 TITLE Primers for synthesizing full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 3663 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
 source 1..816
 /organism="Homo sapiens"
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OY	87	CCCGATGAGCGGCGCCGAGGAAGCAGTCGCGCGCGCCGCGACCCCTGGGGACGGCT	146
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OY	147	CCTGGCTCTGGGCGCGGCGAGAGGGCGAGCCGCACTCTCTTGAGGAGCGGAGTGGAC	206
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OY	387	TGGGAGTATCATCTACTCTGGTGTATCAGGAAGATGAACCGGAACCAACGTGGCATACCT	446
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DB	421	CTAGGATCTTTAAGTGAAGGCAAGGATGACACAAATCTTTGA	468
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DEFINITION	Sequence 8694 from Patent EP1074617.		linear
ACCESSION	AX873789		
VERSION	AX873789.1	GI:40028580	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homio sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.		
JOURNAL	Primers for synthesizing full-length cDNA and their use		
FEATURES	Patent: EP 1074617-A 8694 07-FEB-2001;		
source	Research Association for Biotechnology (JP)		
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Matches 476;	Conservative 0;	Mismatches 1;	Indels 0;
		Gaps 0	
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QY	2245	ACCTCTGAGTGAACCTTCCCGAGAGCCCGGGGCGCAGCCGCCCTCTGGTAGC	2300

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QY	2545	AAAACACAGACATTTATCTATTTTATTTTAAATAGTTGGTGGCTATCTCTCAATRA	2604
Db	143	AAAACACAGACATTTATCTATTTTATTTTAAATAGTTGGTGGCTATCTCTCAATRA	84
QY	2605	GATTTAAATGTCACAAACTGTAGCACAATATATATTTATTTAAATTTCAAAATTGAC	2661
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LOCUS	BD153851		PAT 17-JAN-2003
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD153851		
VERSION	BD153851.1	GI:27859609	
KEYWORDS	JP 2002191363-A/8694.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 518)		
TITLE	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakematsu,A., Nagai,K. and Otsuki,T.		
JOURNAL	Primer for synthesizing full-length cDNA and use thereof		
COMMENT	Patent: JP 2002191363-A 8694 09-JUL-2002; HELIX RESEARCH INSTITUTE		
	OS	Homo sapiens (human)	
	PN	JP 2002191363-A/8694	
	PD	09-JUL-2002	
	PF	28-JUL-2000 JP 20002800990	
	PI	TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO,	
	PI	JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI	
	PC	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10,	
	PC	C12P21/02,C12O1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key	
FEATURES	Location/Qualifiers		
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	1..518	/organism="Homo sapiens"	
	Location/Qualifiers	/mol_type="genomic DNA"	
	Location/Qualifiers	/db_xref="taxon:9606"	
ORIGIN			
Query Match	15.9%	Score 426; DB 6; Length 518;	
Best Local Similarity	99.8%	Pred. No. 5.2e-235;	
Matches	476; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
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QY	2245	ACCTCTGATGATGACCTCTCCCAAGAGCCCGGGGGCCGACGCCCTCTCTGTGTAGC	2304
Db	443	ACCTCTGATGATGACCTCTCCCAAGAGCCCGGGGGCCGACGCCCTCTCTGTGTAGC	384

LOCUS	AC127070	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
Db	2305	GCTGGGGCAGGGCTGTGGTGGCATTCAGAGAGAGACGAAACCTTTCTGTAACTGGCGC	2305						
Db	383	GCTGGGACGGGCTGTGTGGCATTCAGAGAGAGACGAAACCTTTCTGTAACTGGCGC	383						
Qy	2365	CGTCCCGCCGAGAGGGGCGATTTTGTCTTTTGTACATTTTCGAAACTACGTTAAAGC	2365						
Db	323	CGTCCCGCCGAGAGGGGCGATTTTGTCTTTTGTACATTTTCGAAACTACGTTAAAGC	323						
Qy	2425	AGAACTCTGTTTTCAGGAAAAATTTCAGAGGAGAGGCAAGTTATTCAAAAACATGTT	2425						
Db	263	AAAGTCTGTTTTCAGGAAAAATTTCAGAGGAGAGGCAAGTTATTCAAAAACATGTT	263						
Qy	2485	TCAGAGAGAGGAGATATGTTTTCAGGCTTCAGAGAGGATACAAATATCCGCTGCTGGG	2485						
Db	203	TCAGAGAGAGGAGATATGTTTTCAGGCTTCAGAGAGGATACAAATATCCGCTGCTGGG	203						
Qy	2545	AAACCAACAGATTTTATCTATTTTATTTTAAATAGTTTGGTCTATCTTCTAATAA	2545						
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Qy	2605	GATTTAAATGTCACAACTGTAGCACAATATATATTTTAAATTTTAAATTTGAC	2605						
Db	83	GATTTAAATGTCACAACTGTAGCACAATATATATTTTAAATTTTAAATTTGAC	83						
LOCUS <td>AC127070</td> <td>181012 bp</td> <td>DNA</td> <td>linear</td> <td>PRI 28-MAR-2003</td> <td></td> <td></td> <td></td> <td></td>	AC127070	181012 bp	DNA	linear	PRI 28-MAR-2003				
DEFINITION <td colspan="9">Homo sapiens 12 BAC Rpl11-68H1 (Roswell Park Cancer Institute Human BAC Library) complete sequence.</td>	Homo sapiens 12 BAC Rpl11-68H1 (Roswell Park Cancer Institute Human BAC Library) complete sequence.								
ACCESSION <td>AC127070</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	AC127070								
VERSION <td>AC127070.10</td> <td>GI:23343648</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	AC127070.10	GI:23343648							
KEYWORDS <td colspan="9">HTG.</td>	HTG.								
SOURCE <td colspan="9">Homo sapiens (human)</td>	Homo sapiens (human)								
ORGANISM <td colspan="9">Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.</td>	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
REFERENCE <td colspan="9">1 (bases 1 to 181012)</td>	1 (bases 1 to 181012)								
AUTHORS <td colspan="9">Muzny,D.M., Adams,C., Adio-Odoile,B., Ali-osman,F.R., Allen,C., Alldbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P., Bulay,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Garroll,L., Deckerich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Delanew,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabiel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hatt,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulky,S., Hume,J., Ioshikes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korayh,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Liu,C., Liu,W., Louised,H., Lozdo,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Me,J., Maheshwari,M., Mapua,P., Marandel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Maunley,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Monabhat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokweto,S., Ognih,M., Okumou,G., Orzgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshatari,N., Sisson,I.,</td>	Muzny,D.M., Adams,C., Adio-Odoile,B., Ali-osman,F.R., Allen,C., Alldbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P., Bulay,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Garroll,L., Deckerich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Delanew,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabiel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hatt,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulky,S., Hume,J., Ioshikes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korayh,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Liu,C., Liu,W., Louised,H., Lozdo,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Me,J., Maheshwari,M., Mapua,P., Marandel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Maunley,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Monabhat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokweto,S., Ognih,M., Okumou,G., Orzgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshatari,N., Sisson,I.,								


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Query Match 14.4%; Score 386; DB 9; Length 181012;
Best Local Similarity 99.5%; Pred. No. 2e-211;
Matches 616; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 2043 GAAATTCATCATCTCTGTGAACAGACAGAGTTCAAAATGATCCAGAGCCCTGA 2102
DB 108222 GAAATTCATCATCTCTGTGAACAGACAGAGTTCAAAATGATCCAGAGCCCTGA 108281
QY 2103 GCAGCTTCAGACCTGAGGTGAAGAGAGCGTGTTTTAAATACAGACAGACAGCTC 2162
DB 108282 GCAGCTTCAGACCTGAGGTGAAGAGAGCGTGTTTTAAATACAGACAGACAGCTC 108341
QY 2163 AAGGTGTTTCAAGCCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2222
DB 108342 AAGGTGTTTCAAGCCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 108401
QY 2223 TGAATCTTCTGTGAGAGCTTTTAACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2282
DB 108402 TGAATCTTCTGTGAGAGCTTTTAACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 108459
QY 2283 GCAGCCCGCCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2342
DB 108460 GCAGCCCGCCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108519
QY 2343 AAGCTTTTCTGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2402
DB 108520 AAGCTTTTCTGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 108579
QY 2403 TTTTCCGAACTACAGTTAAAGCAGAACTGTTTTCAGAGAGAGAGAGAGAGAGAGAG 2462
DB 108580 TTTTCCGAACTACAGTTAAAGCAGAACTGTTTTCAGAGAGAGAGAGAGAGAGAGAG 108639
QY 2463 CAAGTTATATCAAAAACATGTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2522
DB 108640 CAAGTTATATCAAAAACATGTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108699
QY 2523 TACACATATCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2582
DB 108700 TACACATATCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108759
QY 2583 TTTGGTCTTATCTCTTCAATTAAGTTTAAATGTCACAACTGTCAGCAATTAATATAT 2642
DB 108760 TTTGGTCTTATCTCTTCAATTAAGTTTAAATGTCACAACTGTCAGCAATTAATATAT 108819
QY 2643 TTTATTTTCAAAATGAGC 2661
DB 108820 TTTATTTTCAAAATGAGC 108838

RESULT 24
AC023047 181438 bp DNA linear HTG 05-MAR-2001
LOCUS Homo sapiens chromosome 12 clone RP11-46H11, WORKING DRAFT
DEFINITION AC023047
ACCESSION AC023047
VERSION AC023047.19 GI:9857509
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVIERIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 181438)
AUTHORS Abola,A.P., Bruno,D., Com,L., Dela Rosa,M., Faulkner,D.,

```

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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Center
Center code: SDBTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
Project Information
Center project name: 840
Center clone name: RP11-46H11
----- Summary Statistics -----
Sequencing Vector: M13mp18; X02513
Chemistry: Dye-primer; 1% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178770 bases at least Q40
Consensus quality: 179976 bases at least Q30
Consensus quality: 180370 bases at least Q20
Insert size: 164471; agarose-fp
Insert size: 180938; sum-of-ctnigs
Quality coverage: 10.7x in Q20 bases; agarose-fp
Quality coverage: 9.7x in Q20 bases; sum-of-ctnigs.
NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1 7009: contig of 7009 bp in length
7010 7109: gap of unknown length
7110 23344: contig of 16235 bp in length
23345 23445: gap of unknown length
23445 38890: contig of 15446 bp in length
38891 38990: gap of unknown length
38991 55546: contig of 16556 bp in length
55547 55646: gap of unknown length
55647 103634: contig of 47888 bp in length
103635 181438: gap of unknown length
103635 181438: contig of 77804 bp in length.
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ORIGIN

Query Match 14.4%; Score 386; DB 2; Length 181438;
Best Local Similarity 99.5%; Pred. No. 2e-211;
Matches 616; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

2043 GAAATTCATCATATCTGTGAACAGACAAAGGTTCAAAAATAAGATCCAGAGGCCCTTA 2102
108641 GAAATTCATCATATCTGTGAACAGACAAAGGTTCAAAAATAAGATCCAGAGGCCCTTA 108700
2103 GCAGCTTTCAGACCTGAGAGGTAAGAGAGCGTGTGTTTAAATACAGACAGACAGCGTC 2162
108701 GCAGCTTTCAGACCTGAGAGGTAAGAGAGCGTGTGTTTAAATACAGACAGACAGCGTC 108760
2163 AAGGTGTTTTCACAGCCCTTGAAGGAGAGAGAGCGGTCTCCACAGAGTGTCTGAGG 2222
108761 AAGGTGTTTTCACAGCCCTTGAAGGAGAGAGAGCGGTCTCTCCAGAGTGTCTGAGG 108820
2223 TGACCTTCTGTGAGAGCTTTTACCTCTGAGTGAAGACCTCCAGAGAGCCCGAGGAGG 2282
108821 TGACCTTCTGTGAGAGCTTTTACCTCTGAGTGAAGACCTCCAGAGAGCCCGAGGAGG 108878
2283 GCAGCCCGGCTTCTGTGAGAGCGCTGAGGAGAGCGCTGAGTGAAGACCTCCAGAGAGG 2342
108879 GCAGCCCGGCTTCTGTGAGAGCGCTGAGGAGAGCGCTGAGTGAAGACCTCCAGAGAGG 108938
2343 AAGCTTCTGTGAACATGAGGAGCGCTGAGGAGAGCGGAGGAGGAGGAGGAGGAGGAGG 2402
108939 AAGCTTCTGTGAACATGAGGAGCGCTGAGGAGAGCGGAGGAGGAGGAGGAGGAGGAGG 108998
2403 TTTCGCAAACTACAGTTAAAGAGAGTCTGTTTTCAGAGAAAAGTTTCAAGGAGAGAGG 2462
108999 TTTCGCAAACTACAGTTAAAGAGAGTCTGTTTTCAGAGAAAAGTTTCAAGGAGAGAGG 109058
2463 CAAGTTTATCAAAAACATGTTTTCAGAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 2522
109059 CAAGTTTATCAAAAACATGTTTTCAGAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 109118
2523 TACACAAATATCTGCTGCTGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2582
109119 TACACAAATATCTGCTGCTGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 109178
2583 TTTCGCTTATCTTCTTATTAAGATTTAATGTCACAACTGAGACAAATATATATAT 2642
109179 TTTCGCTTATCTTCTTATTAAGATTTAATGTCACAACTGAGACAAATATATATAT 109238
2643 TTAATAATTTACAAATTGAC 2661
109239 TTAATAATTTACAAATTGAC 109257

RESULT 25
AC023047 181438 bp DNA linear HTG 05-MAR-2001
AC023047/c Homo sapiens chromosome 12 clone RP11-46H11, WORKING DRAFT
DEFINITION
SEQUENCE, 6 unordered pieces.
AC023047
AC023047.19 GI:9857509
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1. (bases 1 to 181438)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Fedorov, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M.,
Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J.,
Yu, S. and Davis, R.W.

JOURNAL REFERENCE AUTHORS

Unpublished
2 (bases 1 to 181438)
Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N.,
Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R.,
Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.,
Yu, S. and Davis, R.W.

TITLE JOURNAL

Direct Submission
Submitted (07-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT

On Aug 19, 2000 this sequence version replaced gi:965109.

----- Genome Center

Center: Stanford DNA Sequencing and Technology Development

Center code: SDSTDC

Web site: <http://sequence-www.stanford.edu/group/human/>

Contact: hum-info@sequence.stanford.edu

----- Project Information

Center project name: 840

Center clone name: RP11-46H11

----- Summary Statistics

Sequencing Vector: M13mp18; X02513

Chemistry: Dye-primer; 1k of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 178770 bases at least Q40

Consensus quality: 179976 bases at least Q30

Consensus quality: 180370 bases at least Q20

Insert size: 164471; agarose-fp

Insert size: 180938; sum-of-coverage

Quality coverage: 10.7x in Q20 bases; agarose-fp

Quality coverage: 9.7x in Q20 bases; sum-of-coverage.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 7009: contig of 7009 bp in length

* 7010 7109: gap of unknown length

* 7110 23444: contig of 16235 bp in length

* 23445 23445: gap of unknown length

* 23445 38890: contig of 15446 bp in length

* 38891 38890: gap of unknown length

* 38891 55546: contig of 16556 bp in length

* 55547 55547: gap of unknown length

* 55547 103534: contig of 47888 bp in length

* 103535 103634: gap of unknown length

* 103635 181438: contig of 77804 bp in length.

FEATURES

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ORIGIN

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			Indels	0	Gaps	0
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DEFINITION	sgm1101345 Human DNA (sequenom) tagged site.				
ACCESSION	BV180578				
VERSION	BV180578				
KEYWORDS	BV180578.1	GI:48017719			
SOURCE	STS.				
ORGANISM	Homo sapiens				
	Homo sapiens (human)				
	Homo sapiens				

REFERENCE

AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.

TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene

TITLE

Regions
Genome Res. (2004) In press

COMMENT

Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS site: 756.

FEATURES

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ACCESSION	BV168191				
VERSION	BV168191.1	GI:48001924			
KEYWORDS	STS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE

AUTHORS	TITLE	JOURNAL
NEALSON, K.M., WERNERLEIN, G., KAMMERER, S., ROYAL, C.K., SHU, M.M., CANTOR, C.R. and BRAUN, A.	Large-Scale Validation of Single Nucleotide Polymorphisms in Genomic Regions	Genome Res. (2004) In press

TITLE

JOURNAL
Genome Res. (2004) In press
COMMENT

COMMENT

Contact: Andreas Brian
Pharmaceuticals division
Sequenom, Inc.
3555 John Hopkins Court, San Diego, CA 92121, USA
Tel.: 1858/2025018
Fax: 1858/2025020
Email: abrian@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 601.

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RESULT 28

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LOCUS				
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ACCESSION	AX385952			
VERSION	AX385952.1	GI:19579082		
KEYWORDS	.			

RESULT 28

AX385952/c	AX385952	617 bp	DNA	linear	PAT 19-MAR-2002
LOCUS	Sequence	880	from Patent WO0214500.		
DEFINITION	AX385952				
ACCESSION	AX385952				
VERSION	AX385952.1	GI:19579082			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Escobedo, J., Garcia, P. D., Sudduth-Klinger, J., Reinhard, C.,				
	Radazzo, F., Lamson, G., Scott, E. M., Zhang, G., Kaessan, A., Pot, D. and				
	Labat, I.				
TITLE	Human genes and gene expression products				
JOURNAL	Patent: WO 0214500-A 880 21-PEB-2002; (US)				
	CHIRON CORPORATION (us); Hyseq Inc. (US)				
FEATURES	Location/Qualifiers				
	1..617				
SOURCE	/organism="Homo sapiens"				

* by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 158897: contig of 158897 bp in length.

FEATURES
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 Location/Qualifiers
 1. 158897
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone_lib="RP24-374B14"
 /clone_1lb="RPC1-24 Male Mouse BAC"

ORIGIN

Query Match 1.4%; Score 38; DB 2; Length 158897;
 Best Local Similarity 100.0%; Pred.No. 4.7e-09;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1975 GTACATCCCGCTCTGACTGCTACTGAGCGCGTAACTG 2012

Db 40304 GTAACTCCGCTCTGACTGCTACTGAGCGCGTAACTG 40341

RESULT 31
 BC049792 3194 bp mRNA linear ROD 30-JUN-2004
 LOCUS BC049792
 DEFINITION Mus musculus checkpoint with forkhead and ring finger domains, mRNA
 (CDNA clone MGC:59419 IMAGE:6510480), complete cds.
 ACCESSION BC049792.1 GI:29437110
 VERSION BC049792.1
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 1 (bases 1 to 3194)

Krausberg R.L., Collins F.S., Wagner L., Shenn C.M., Schlier G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L.,
 Scheetz T.E., Brownstein M.J., Ueding T.B., Toshiyuki S.,
 Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.,
 Abramson R.D., Muliyil S.J., Bosak S.A., McManus P.J.,
 McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S.,
 Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y.,
 Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D.,
 Dickson M.C., Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S., Krzywinski M.I., Skalska U., Smalish D.B.,
 Schnerch A., Schein J.E., Jones S.J. and Marra M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
 PUBLISHED
 REFERENCE
 TITLE
 AUTHORS
 JOURNAL

REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgaps-remail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca

FEATURES

source

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
 Featherstone, Malachi Griffith, Oji Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lila Prabhu,
 Parvaneh Saeedi, JR Santos, Angeliq Schnerch, Ursula Skalska,
 Duane Smalish, Jeff Scott, Miranda Tsai, George Yang, Jacqie
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 109 Row: 1 Column: 17
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 27370049.

Location/Qualifiers

1. 3194
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="MGC:59419 IMAGE:6510480"
 /issue_type="limb, mouse, day 10.5 and 11.5, pool of
 undifferentiated limb containing undifferentiated limb
 mesenchyme and early condensing mesenchyme."
 /clone_1lb="NIH MGC_134"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6.1"
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 /gene="Cnfr"
 /note="synonyms: RNF116, C230082M18"
 /db_xref="LOCUSID:231600"
 /db_xref="MGI:2444898"
 71. 2065
 /gene="Chfr"
 /product="checkpoin with forkhead and ring finger
 domains"
 /protein_id="AAH49792.1"
 /db_xref="GI:29437111"
 /db_xref="LOCUSID:231600"
 /db_xref="MGI:2444898"
 /translation="MEHGEBOPEPPEPWGRLRLGAEDEPOILLMREWTGRR
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 IYLVAKTBNHNVAVLYESLSGKSLTQDSLEANKENHVTXKDSGPGQDPQVP
 ILSPVAKTLEBPQPSSTSDILPASTSTREBELTSAQKSSSGSPGNTSIPGR
 SSVANGLSISLSPVQDKASFTSLSEKHELEPAKRMKDEGLTNLQILVSG
 RNAQVSSSEVDVDAVSPKMEETLTCILQDLHDVSLQCMHTFCACYSQWER
 SSICPTCRCPVPERICNHLINLVEAYLIQHPDKSEEDVSMARNTITDMLQPK
 VRRSFDEGSEEDLLESDVSESDISDIPTVCRCQCEYRQAVQSIPVPESEL
 GTALIGERAPSTASLPTAAPDWCPIQSHAICTCCPQMPDRABEOPRVAPO
 QCAVCIQPCCHLYMGCTRTGCGCLAPFELNIDKCLDGVANNYBEDIKNYIAT
 RGLTWKSVITSESLALQGVFPMISDRITGNTVLCYCGALRSFRELTYOIRONTIPASE
 LPVTWSPRDVCYWGRCRQVFAHAKMFNHI CEOTRFN"

CDS

ORIGIN

Query Match 1.4%; Score 37; DB 10; Length 3194;
 Best Local Similarity 100.0%; Pred.No. 1.1e-08;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TTCCCGAGCAATTAAGTGTCTCTGAGATCACTGTA 274
 Db 218 TTCCCGAGCAATTAAGTGTCTCTGAGATCACTGTA 254

RESULT 32

LOCUS AC087142 321708 bp DNA linear HTG 09-DEC-2000.
 DEFINITION Mus musculus clone RP23-211L19, WORKING DRAFT SEQUENCE, 65
 unordereed pieces.

ACCESSION AC087142
 VERSION AC087142.1 GI:11610868
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Mouse
AUTHORS Unpublished
REFERENCE 2 (bases 1 to 321708)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1818179
Center clone name: RPCI-23_211119

Summary Statistics
Consensus quality: 271436 bases at least Q40
Consensus quality: 288232 bases at least Q30
Consensus quality: 297606 bases at least Q20
Estimated insert size: 231000; agarose-fp estimation
Estimated insert size: 315308; sum-of-contigs estimation
Quality coverage: 6.76 in Q20 bases; agarose-fp estimation
Quality coverage: 4.95 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1059: contig of 1059 bp in length
* 1060 1159: gap of unknown length
* 1160 2435: contig of 1276 bp in length
* 2436 2535: gap of unknown length
* 2536 3565: contig of 1030 bp in length
* 3566 3665: gap of unknown length
* 3666 4694: contig of 1029 bp in length
* 4695 4794: gap of unknown length
* 4795 6024: contig of 1230 bp in length
* 6025 6124: gap of unknown length
* 6125 7295: contig of 1171 bp in length
* 7296 7395: gap of unknown length
* 7396 8587: contig of 1192 bp in length
* 8588 8687: gap of unknown length
* 8688 10043: contig of 1356 bp in length
* 10044 10143: gap of unknown length
* 10144 11453: contig of 1310 bp in length
* 11454 11553: gap of unknown length
* 11554 12767: contig of 1214 bp in length
* 12768 12867: gap of unknown length
* 12868 14070: contig of 1203 bp in length
* 14071 14170: gap of unknown length
* 14171 15238: contig of 1068 bp in length
* 15239 15338: gap of unknown length
* 15339 16901: contig of 1563 bp in length
* 16902 17001: gap of unknown length
* 17002 18477: contig of 1476 bp in length
* 18478 18577: gap of unknown length
* 18578 20010: contig of 1433 bp in length
* 20011 20110: gap of unknown length
* 20111 21739: contig of 1629 bp in length
* 21740 21839: gap of unknown length
* 21840 24230: contig of 2391 bp in length
* 24231 24330: gap of unknown length
* 24331 26064: contig of 1734 bp in length
* 26065 26164: gap of unknown length
* 26165 27278: contig of 1114 bp in length

* 27279 27378: gap of unknown length
* 27379 29439: contig of 2061 bp in length
* 29440 29539: gap of unknown length
* 29540 32551: contig of 2812 bp in length
* 32552 32451: gap of unknown length
* 32452 34348: contig of 1897 bp in length
* 34349 34448: gap of unknown length
* 34449 36449: contig of 2001 bp in length
* 36450 36549: gap of unknown length
* 36550 37925: contig of 1376 bp in length
* 37926 38025: gap of unknown length
* 38026 39788: contig of 1763 bp in length
* 39789 39888: gap of unknown length
* 39889 42604: contig of 2716 bp in length
* 42605 42704: gap of unknown length
* 42705 44712: contig of 2008 bp in length
* 44713 44812: gap of unknown length
* 44813 47566: contig of 2754 bp in length
* 47567 47666: gap of unknown length
* 47667 49373: contig of 1707 bp in length
* 49374 49473: gap of unknown length
* 49474 52688: contig of 3215 bp in length
* 52689 52788: gap of unknown length
* 52789 56081: contig of 3293 bp in length
* 56082 56181: gap of unknown length
* 56182 59381: contig of 3200 bp in length
* 59382 59481: gap of unknown length
* 59482 61906: contig of 2425 bp in length
* 61907 62006: gap of unknown length
* 62007 64488: contig of 2482 bp in length
* 64489 64588: gap of unknown length
* 64589 65829: contig of 1241 bp in length
* 65830 65929: gap of unknown length
* 65930 68055: contig of 2126 bp in length
* 68056 68155: gap of unknown length
* 68156 72511: contig of 4356 bp in length
* 72512 72611: gap of unknown length
* 72612 76828: contig of 4217 bp in length
* 76829 76928: gap of unknown length
* 76929 80537: contig of 3609 bp in length
* 80538 80637: gap of unknown length
* 80639 86510: contig of 5873 bp in length
* 86511 86610: gap of unknown length
* 86611 88767: contig of 2157 bp in length
* 88768 88867: gap of unknown length
* 88868 91586: contig of 2719 bp in length
* 91587 91686: gap of unknown length
* 91687 96792: contig of 5106 bp in length
* 96793 96892: gap of unknown length
* 96893 102331: contig of 5339 bp in length
* 102332 102331: gap of unknown length
* 102332 106317: contig of 3986 bp in length
* 106318 106417: gap of unknown length
* 106418 111040: contig of 4623 bp in length
* 111041 111140: gap of unknown length
* 111141 116735: contig of 5595 bp in length
* 116736 116835: gap of unknown length
* 116836 120801: contig of 3966 bp in length
* 120802 120901: gap of unknown length
* 120902 127537: contig of 6636 bp in length
* 127538 127637: gap of unknown length
* 127638 133314: contig of 5677 bp in length
* 133315 133414: gap of unknown length
* 133415 139072: contig of 5658 bp in length
* 139073 139172: gap of unknown length
* 139173 143714: contig of 4542 bp in length
* 143715 143814: gap of unknown length
* 143815 151343: contig of 7529 bp in length
* 151344 151443: gap of unknown length
* 151444 160187: contig of 8744 bp in length
* 160188 160287: gap of unknown length
* 160288 168688: contig of 8401 bp in length
* 168689 168788: gap of unknown length

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* 168789 177395: contig of 8607 bp in length
* 177396 177495: gap of unknown length
* 177496 189516: contig of 12021 bp in length
* 189517 189616: gap of unknown length
* 189616 204042: contig of 14426 bp in length
* 204043 204142: gap of unknown length
* 204143 214352: contig of 10210 bp in length
* 214353 214452: gap of unknown length
* 214453 225667: contig of 11215 bp in length
* 225668 225767: gap of unknown length
* 225768 245517: contig of 19750 bp in length
* 245518 259483: contig of 13866 bp in length
* 259484 259583: gap of unknown length
* 259584 272039: contig of 12456 bp in length
* 272040 272139: gap of unknown length
* 272140 292269: contig of 20130 bp in length
* 292270 321708: contig of 29339 bp in length.
* 292370 321708: contig of 29339 bp in length.
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FEATURES
source
1. .321708
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-21119"

ORIGIN
/clone_11b="RP23 mouse BAC library 23"

Query Match 1.4%; Score 37; DB 2; Length 321708;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TTCCCGACGATTAAGTGTCTCTGAGATCACTGTA 274
DB 202208 TTCCCGACGATTAAGTGTCTCTGAGATCACTGTA 202244

RESULT 33
AC087159 338116 bp DNA linear HTG 09-DEC-2000
LOCUS AC087159
DEFINITION Mus musculus clone RP23-69F2, WORKING DRAFT SEQUENCE, 56 unordered
pieces.
AC087159.1 GI:11610885
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 338116)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 338116)
REFERENCE DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1763490
Center clone name: RP23-69F2

Summary Statistics
Consensus quality: 297593 bases at least Q40
Consensus quality: 310387 bases at least Q30
Consensus quality: 317713 bases at least Q20
Estimated insert size: 24100; agarose-fp estimation
Estimated insert size: 332616; sum-of-contigs estimation

Quality coverage: 8.79 in Q20 bases; agarose-fp estimation
Quality coverage: 6.37 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```
1 1568: contig of 1568 bp in length
1569 1669: gap of unknown length
1669 2704: contig of 1036 bp in length
2705 2804: gap of unknown length
2805 4009: contig of 1205 bp in length
4010 4109: gap of unknown length
4110 5400: contig of 1291 bp in length
5401 5501: gap of unknown length
5501 6793: contig of 1293 bp in length
6794 6893: gap of unknown length
6894 8357: contig of 1464 bp in length
8358 8457: gap of unknown length
8458 9961: contig of 1503 bp in length
9961 10060: gap of unknown length
10061 11179: contig of 1119 bp in length
11180 11279: gap of unknown length
11280 12550: contig of 1271 bp in length
12551 12650: gap of unknown length
12651 14127: contig of 1477 bp in length
14128 14227: gap of unknown length
14228 15366: contig of 1139 bp in length
15367 15466: gap of unknown length
15467 16821: contig of 1355 bp in length
16822 16921: gap of unknown length
16922 18499: contig of 1578 bp in length
18500 18599: gap of unknown length
18600 19737: contig of 1138 bp in length
19738 19837: gap of unknown length
19838 22127: contig of 2290 bp in length
22128 22227: gap of unknown length
22228 24753: contig of 2526 bp in length
24754 24853: gap of unknown length
24854 26957: contig of 2104 bp in length
26958 27057: gap of unknown length
27058 30024: contig of 2967 bp in length
30025 30124: gap of unknown length
30125 32739: contig of 2515 bp in length
32740 34710: gap of unknown length
34711 34810: contig of 1971 bp in length
34811 38720: contig of 3910 bp in length
38721 38820: gap of unknown length
38821 42085: contig of 3265 bp in length
42086 42185: gap of unknown length
42186 45949: contig of 3764 bp in length
45950 46049: gap of unknown length
46050 49056: contig of 3007 bp in length
49057 49156: gap of unknown length
49157 51327: contig of 2171 bp in length
51328 51427: gap of unknown length
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55025 57807: contig of 2783 bp in length
57808 57907: gap of unknown length
57909 59837: contig of 1930 bp in length
59838 59937: gap of unknown length
59939 63506: contig of 3569 bp in length
63507 63606: gap of unknown length
63607 65893: contig of 2287 bp in length
65894 65994: gap of unknown length
65995 68320: contig of 2327 bp in length
68321 70667: gap of unknown length
70668 70667: contig of 2447 bp in length
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* 70968 70967: gap of unknown length
* 70968 73224: contig of 2257 bp in length
* 73325 73324: gap of unknown length
* 79062 79062: contig of 5738 bp in length
* 79063 79162: gap of unknown length
* 79163 85875: contig of 6713 bp in length
* 85876 85975: gap of unknown length
* 85976 93569: contig of 7594 bp in length
* 93570 93670 100230: contig of 6561 bp in length
* 100231 100330: gap of unknown length
* 100331 110643: contig of 10313 bp in length
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* 119248 128090: contig of 8843 bp in length
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* 142079 142178: gap of unknown length
* 142179 152214: contig of 10036 bp in length
* 152215 152314: gap of unknown length
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* 158337 158736: gap of unknown length
* 158737 167288: contig of 8552 bp in length
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* 177586 191370: contig of 13785 bp in length
* 191371 191470: gap of unknown length
* 191471 204484: contig of 13014 bp in length
* 204485 209828: contig of 5244 bp in length
* 209829 209928: gap of unknown length
* 209929 224035: contig of 14107 bp in length
* 224036 224135: gap of unknown length
* 224136 238966: contig of 14831 bp in length
* 238967 239066: gap of unknown length
* 239067 25264: contig of 16198 bp in length
* 25265 255364: gap of unknown length
* 255365 257695: contig of 12331 bp in length
* 257696 267795: gap of unknown length
* 267796 286490: contig of 18695 bp in length
* 286491 286590: gap of unknown length
* 286591 307496: contig of 20906 bp in length
* 307497 338116: gap of unknown length
* 307597 338116: contig of 30520 bp in length.

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FEATURES
SOURCE
1. 338116
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-69F2"
/clone_1b="RPM1 mouse BAC library 23"

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ORIGIN

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Query Match 1.4%; Score 37; DB 2; Length 338116;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 238 TTCGCCAGCAATTAAGTGTCTCTGAGATCACTGTA 274

Db 189868 TTCGCCAGCAATTAAGTGTCTCTGAGATCACTGTA 189904

```

RESULT 34
AC125898/c 202792 bp DNA linear HTG 15-NOV-2002
LOCUS Rattus norvegicus clone CH230-314P18, *** SEQUENCING IN PROGRESS
DEFINITION *** 7 unoverlapped pieces.
AC125898
AC125898.3 GI:25008623

```

```

KEYWORDS
SOURCE HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
ORGANISM Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 202792)
REFERENCE
AUTHORS Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrechts, S., Anin, A., Anguiano, D.,
Ayalebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bernhamed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, T., Cestari, H., Ceter, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Dayla, M.L., Davis, C., Davy-Carroll, L., De Ande, C., Dederich, D.,
Delgado, O., Denon, S., Derramo, C., Ding, Y., Dinh, H., Divya, K.,
Draeger, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunnarone, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,
Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A.,
Karpas, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshewa, L., Louised, H., Lorado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahidatane, M., Mamoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, B.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwackeleme, O., Okwom, G., Olarunpaagun, A., Pal, S., Parke, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C.,
Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.,
Puzo, M., Quito, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodery, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smjs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlezyk, R., Woodson, H., Wolley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von
Neiderhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission

```

```

TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202792)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 202792)
REFERENCE Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

```

COMMENT

On Nov 15, 2002 this sequence version replaced gi:23807727.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GWMO

Center clone name: CH230-314P18

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 166637 bases at least Q40

Consensus quality: 168395 bases at least Q30

Consensus quality: 169698 bases at least Q20

Estimated insert size: 172322; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbankdraftdata.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 163896: contig of 163896 bp in length

* 16397 163995: gap of unknown length

* 16397 170075: contig of 6079 bp in length

* 170076 170175: gap of unknown length

* 170176 173847: contig of 3672 bp in length

* 173848 173947: gap of unknown length

* 173948 177191: contig of 3244 bp in length

* 177192 177291: gap of unknown length

* 177292 178689: contig of 1398 bp in length

* 178690 178789: gap of unknown length

* 178790 180421: contig of 1632 bp in length

* 180422 180521: gap of unknown length

* 180522 202792: contig of 22271 bp in length.

FEATURES

Source

1. 202792

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-314P18"

29992..31901

/note="wgs_end_extension"

clone_end:T7"

104416..104486

/note="clone_boundary"

clone_end:T7"

site:

end_sequence:BZ249453"

122630..127621

/note="clone boundary"

clone_end:Sp6

site:

end_sequence:BZ249454"

163997..165926

/note="wgs_end_extension"

clone_end:Sp6"

167885..170075

/note="wgs_end_extension"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 34; DB 2; Length 202792;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGCAATTAAGTGTCTGTGAGATCACTGTA 274

DB 86522 CCCAGCAATTAAGTGTCTGTGAGATCACTGTA 86489

RESULT 35

BY002855

LOCUS

DEFINITION S2088639RFL1.T0 12961/SVIMJ Mus musculus STS genomic, sequence

tagged site.

ACCESSION BY002855

VERSION BY002855.1 GI:22755932

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Kerstin Lindblad-Toh

Whitehead Institute for Biomedical Research, Center for Genome

Research

320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172521477

Fax: 6172580903

Email: kersti@genome.wi.mit.edu

Primer A: None

Primer B: None

STS size: 601

Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads

were generated from 129S1/SVIMJ, C3H/HeJ, and BALB/cByJ. The WGS

reads were placed uniquely on the MGSVC3 C57BL/6J assembly and SNP

detection was carried out by SSHA-SNP. 225,000 reads were

annotated

as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J

and the strain from which the particular read came. The validation

rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers

1..601

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129S1/SVIMJ"

/db_xref="taxon:10090"

/map="4 5 22-555 107871915-107872448"

/clone_11b="129S1/SVIMJ"

<1..>601

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 32; DB 11; Length 601;

Matches 100.0%; Pred. No. 7.1e-06;


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* 28550 33402: contig of 4853 bp in length
* 33403 33502: gap of unknown length
* 33503 37568: contig of 4066 bp in length
* 37569 37668: gap of unknown length
* 42544 42544: contig of 4876 bp in length
* 42645 42645: gap of unknown length
* 47232 47232: contig of 4587 bp in length
* 47332 52835: gap of unknown length
* 52836 52935: contig of 5504 bp in length
* 52936 59373: gap of unknown length
* 59374 59473: contig of 6438 bp in length
* 59474 66585: contig of 7112 bp in length
* 66586 66685: gap of unknown length
* 66686 74608: contig of 7923 bp in length
* 74609 75327: gap of unknown length
* 75328 75427: contig of 619 bp in length
* 75428 76074: contig of 647 bp in length
* 76075 76174: gap of unknown length
* 76175 81491: contig of 5317 bp in length
* 81492 81591: gap of unknown length
* 81592 88018: contig of 6427 bp in length
* 88019 98670: contig of 10552 bp in length
* 98671 98770: gap of unknown length
* 98771 113277: contig of 14507 bp in length
* 113278 127626: contig of 14249 bp in length
* 127627 127726: gap of unknown length
* 127727 146516: contig of 18790 bp in length.

```

FEATURES

source

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1. 146516
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-21506"
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1270. 2651
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misc_feature
2752. 4398
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4499. 5398
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6039. 8062
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misc_feature
8163. 10520
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10621. 13358
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13459. 15803
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21498. 25904
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42645. 47231
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47332. 52835
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52936. 59373

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ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 146516;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2652 ACBAATTGACAAAAA 2679

Db

102453 ACBAATTGACAAAAA 102426

RESULT 38

AC126634

LOCUS 218226 bp DNA linear HTG 15-NOV-2002

DEFINITION Rattus norvegicus clone CH230-13813, WORKING DRAFT SEQUENCE.

AC126634

VERSION AC126634.4 GI:25007898

KEYWORDS

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Rattus norvegicus

Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

AUTHORS

1 (bases 1 to 218226)
Muzny,D,Macie, Metzker,M, Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amth, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Butch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Crease, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Hayes, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gervaz, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, B., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Koyar, C., Kowis, C., Kraft, C. L., Lebow, H., Levam, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuwa, L., Louieged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Mallory, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,

Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodegref, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Stemle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valsas, R., Vera, V., Villaseña, D., Waldron, L., Walker, B., Wang, Q.,
Wang, G., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willison, R., Wlezyk, R., Wooder, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhuesern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 228987)
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 228987)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265947.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
<http://www.hgsc.bcm.tmc.edu/projects/rat/>. Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

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misc_feature
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/db_xref="taxon:10116"
/mol_type="genomic DNA"
/organism="Rattus norvegicus"
location/offsets
1. .228987
source
IRES
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Query Match	1.0%	Score 28	DB 2	Length 228987
Best Local Similarity	100.0%	Pred. No. 0.0032		
Matches 28	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	2652	ACAAATTGACAAAAAAAAAAAAAAAAA	2679	
Db	6876	ACAAATTGACAAAAAAAAAAAAAAAAA	6849	

REFERENCE	1 (bases 1 to 274796)
AUTHORS	Muzny, D. Marie., Metckler, M. Lee., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alstrokes, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Bace, E., Bader, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnesread, M., Benahmed, F., Blawolo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cessari, H., Centar, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Derich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dith-H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dublin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabler, A., Gante, K., Garcia, A., Garneri, F., Garza, M., Gedroegge, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Huliyar, S., Hume, J., Idebrard, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Lervan, J., Lewis, L., Li, Z., Liu, J., Liu, U., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenswale, L., Loulsegod, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, P., McNeill, T. Z., Meener, E., Mloaavljevic, A., Miner, G., Minda, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwachukwu, S., Okunonu, G., Olariupungson, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plamackoch, C.,

Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rivers, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Riz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, U., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wiczek, R., Woden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, U., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 274796)
Worley, K.C.

Direct Submission
Submitted (21-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 274796)
Rat Genome Sequencing Consortium.

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25009660. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rac/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GPUL
Center clone name: CH230-86C24

----- Summary Statistics
Assembly program: Atlas 3.0
Consensus quality: 262493 bases at least Q40
Consensus quality: 263877 bases at least Q30
Consensus quality: 264932 bases at least Q20
Estimated insert size: 270537; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 271424: contig of 271424 bp in length
* 271425 271524: gap of unknown length
* 271525 272554: contig of 1030 bp in length

272555 272654: gap of unknown length
* 272655 273674: contig of 1020 bp in length
* 273675 273774: gap of unknown length
* 273775 274796: contig of 1022 bp in length.

FEATURES
source
1..274796
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-86C24"
1..1265
/note="wgs_contig"

ORIGIN
misc_feature

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 274796;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2652 ACMAATTGACMAAAAAAAAAAAAAAAAAAAAA 2679
|||||
Db 75393 ACMAATTGACMAAAAAAAAAAAAAAAAAAAAA 75366

RESULT 41
AC117568 167166 bp DNA linear HTG 27-AUG-2002
LOCUS
AC117568
DEFINITION
Mus musculus clone RP24-51J14, WORKING DRAFT SEQUENCE, 4 unordered pieces.
AC117568.3 GI:22507215
VERSION
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORIGIN
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 167166)
Unpublished
1 (bases 1 to 167166)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J., Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Dietz, U.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatae, A., Kelle, C., Lacroque, K., Lamazares, R., Landers, T., Lenoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, U., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Recta, R., Rieback, M., Riley, R., Riese, C., Rogov, P., Roman, N., Roselt, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 167166)
Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Camarata, U., Chang, U., Chararo, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, U.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (27-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 27, 2002 this sequence version replaced gi:22296976.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L21336

Center clone name: 511.J.14

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 165942 bases at least Q40

Consensus quality: 166212 bases at least Q30

Consensus quality: 166486 bases at least Q20

Insert size: 163000; agarose-ef

Insert size: 166866; sum-of-coverage

Quality coverage: 12.9 in Q20 bases; agarose-ef

Quality coverage: 12.6 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 18065: contig of 18065 bp in length
* 18066 18165: gap of 100 bp
* 18166 24868: contig of 6703 bp in length
* 24869 24968: gap of 100 bp
* 24969 71883: contig of 46915 bp in length
* 71884 71983: gap of 100 bp
* 71984 167166: contig of 95183 bp in length.

FEATURES

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/db_xref="taxon:10090"

/clone="RP24-511J14"
/clone_lib="RP24 Male Mouse BAC"

misc_feature

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24969..71883
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0;
Matches 27; Conservative 0; Indels 0; Gaps 0;
2653 CAAATTGACAAAAA 2679
60190 CAAATTGACAAAAA 60216

RESULT 42

AC115904

LOCUS

DEFINITION

AC115904

AC115904.13

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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JOURNAL

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AUTHORS

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

AC115904 167938 bp DNA linear ROD 03-MAR-2004
Mus musculus chromosome 16, clone RP24-472P22, complete sequence.
AC115904
AC115904.13 GI:44891105
HTG.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 167938)
Birten, B., Nussbaum, C. and Landers, E.
Unpublished
2 (bases 1 to 167938)
Birten, B., Linton, L., Nussbaum, C., Landers, E., Ali, A., Allen, N.,
Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goette, M., Graham, L., Grand-Pierre, N.,
Hagob, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Laskocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, D., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 167938)
Birten, B., Nussbaum, C., Landers, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barina, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K.,
Diaz, J., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hagez, N., Hasopjan, D., Hagob, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, E., Levine, R.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Scudis, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission


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26449..26560      /rpt_family="L1"
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26981..27103      /rpt_family="Alu"
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27126..27238      /rpt_family="MALR"
repeat_region      /rpt_family="Alu"
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37870..37913      /rpt_family="B4"
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40864..41239      /rpt_family="ERV1"
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46290..46389      /rpt_family="L2"
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48112..48613      /rpt_family="MALR"
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49627..50013      /rpt_family="MALR"
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50710..50882      /rpt_family="MER2_type"
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50890..51030      /rpt_family="MER2_type"
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51031..51192      /rpt_family="Achoho"
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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2653 CAAATTGACAAAAA 2679
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DB      49641 CAAATTGACAAAAA 49615

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RESULT 44
LOCUS   AC123851
DEFINITION Mus musculus BAC clone RP23-323K4 from chromosome 16, complete
      230221 bp DNA linear ROD 11-NOV-2003

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sequence.
AC123851
VERSION AC123851.4 GI:28376830
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 230221)
Shah, N., Kozlowicz, A., and Schatzkammer, K.
The sequence of Mus musculus BAC clone RP23-323K4
Unpublished (2001)
2 (bases 1 to 230221)
Wilson, R.
Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 230221)
McPherson, J.D. and Waterson, R.H.
Direct Submission
Submitted (01-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 230221)
McPherson, J.D. and Waterson, R.H.
Direct Submission
Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 230221)
McPherson, J.D. and Waterson, R.H.
Direct Submission
Submitted (14-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 230221)
Wilson, R.
Direct Submission
Submitted (11-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 14, 2003 this sequence version replaced gi:23228091.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BA0323K04

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:
The RP23-323 BAC library has been constructed by Kazuhiro Osewaga and Minako Tateo in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone.

FEATURES
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/map="16"
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/clone_lib="RPCI-23"
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182. .339
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363. .431
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432. .452
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1466. .1578
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1900. .2161
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2976. .3162
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3376. .3473
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/rpt_family="Alu"
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3805. .4093
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5306. .5460
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5486. .5756
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5947. .6185
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6193. .6274
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6275. .6421
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6422. .6564
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6835. .6908
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repeat_region 13350. .13469
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repeat_region 15276. .15865
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Best Local Similarity 100.0%; Pred No. 0.012; DB 10; Length 230221;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2653 CAAATTGACCAAAAAAAAAAAAAAAAAA 2679
Db 221953 CAAATTGACCAAAAAAAAAAAAAAAAAA 221927

RESULT 45
AL772311/c 234393 bp DNA linear ROD 08-AUG-2003
LOCUS Mouse DNA sequence from clone RP23-87P16 on chromosome 4, complete
DEFINITION sequence.
ACCESSION AL772311
VERSION AL772311.19 GI:33412257
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 234393)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE Direct Submission
 JOURNAL Submitted (08-AUG-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 COMMENT On Aug 1, 2003 this sequence version replaced gi:33386469. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-87P16 is from the RPI-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

FEATURES
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 1. 234393
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="4"
 /clone="RP23-87P16"
 /clone_1fb="RPI-23"

ORIGIN

Query Match 1.0%; Score 27; DB 10; Length 234393;
 Best Local Similarity 100.0%; Pred.No. 0.012;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2653 CAAATTGACAAAAA 2679
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 Db 201585 CAAATTGACAAAAA 201559

RESULT 46
 AC102564/c 239783 bp DNA linear HTG 10-JUL-2003
 LOCUS Mus musculus clone RP23-210C12, WORKING DRAFT SEQUENCE, 6 unordered
 DEFINITION pieces.
 AC102564
 AC102564.3 GI:32490706
 VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 239783)

AUTHORS Birren, B., Nusbaum, C. and Lander, E.
 TITLE Mus musculus, clone RP23-210C12
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 239783)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Brown, A., Camarata, V., Campilano, A., Chang, J., Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dods, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardys, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Hearford, A., Horton, L., Hulme, W., Illiv, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, D., Margulis, N., Matthews, J., McCarthy, M., McEwan, P., McKernan, K., McSheehy, R., Meldrum, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhng, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J., Vasiliiev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
 JOURNAL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 239783)
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choquet, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dods, S., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardys, S., Graham, L., Grand-Pierre, N., Hafe, N., Hagopian, D., Hagos, B., Hall, V., Horton, L., Hulme, W., Illiv, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhng, P., Pierre, N., Rachupka, A., Ramasamy, V., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vasiliiev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (10-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 10, 2003 this sequence version replaced gi:2281552.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WtBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center Project name: L19015
 Center clone name: 210 C_12
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 238594 bases at least Q40
 Consensus quality: 238993 bases at least Q30
 Consensus quality: 239154 bases at least Q20
 Insert size: 212000; agarose-fp

Insert size: 239283; sum-of-coverage
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.5 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 5588: contig of 5588 bp in length
5689 5689: gap of 100 bp
90331 90331: contig of 84643 bp in length
90432 90432: gap of 100 bp
120455 120455: contig of 30024 bp in length
120456 120456: gap of 100 bp
120555 120555: contig of 44829 bp in length
120556 120556: gap of 100 bp
165385 165385: gap of 100 bp
165485 165485: contig of 62333 bp in length
228023 228023: gap of 100 bp
228123 228123: contig of 11660 bp in length.
228124 228124: contig of 11660 bp in length.

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90432 90432: gap of 100 bp
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120555 120555: contig of 44829 bp in length
120556 120556: gap of 100 bp
165385 165385: gap of 100 bp
165485 165485: contig of 62333 bp in length
228023 228023: gap of 100 bp
228123 228123: contig of 11660 bp in length.
228124 228124: contig of 11660 bp in length.

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1. 5588
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5689 5689: gap of 100 bp
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120555 120555: contig of 44829 bp in length
120556 120556: gap of 100 bp
165385 165385: gap of 100 bp
165485 165485: contig of 62333 bp in length
228023 228023: gap of 100 bp
228123 228123: contig of 11660 bp in length.
228124 228124: contig of 11660 bp in length.

ORIGIN

Query Match 1.0%; Score 27; DB 2; Length 239783;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2653 CAAATTGACAAAAA 2679
DB 168024 CAAATTGACAAAAA 167998

RESULT 47

AC129762 266632 bp DNA linear HTG 09-NOV-2002
LOCUS Rattus norvegicus clone CH230-42A2, WORKING DRAFT SEQUENCE, 2
DEFINITION
AC129762
unordered pieces.
AC129762.3 GI:24635717
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

REFERENCE
1 (bases 1 to 266632)
AUTHORS Muzny, D., Marle, M., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrechts, S., Amin, A., Anguiano, D., Anyalebechi, V., Ayvaz, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhamed, F.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (02-NOV-2002) Human Genome Sequencing Center. Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 266632)
Rat Genome Sequencing Consortium.
Submitted (09-NOV-2002) Human Genome Sequencing Center. Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 6, 2002 this sequence version replaced g1:2326431.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Biswal, K., Blair, J., Blankenburg, K., Blych, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Caldeon, E., Cardenas, V., Carter, K., Cavazos, I., Cessari, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dedrich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Din, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duva, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabril, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Gilly, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenzulewa, L., Louieged, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okunogun, G., Olundunsgoon, A., Pal, S., Pasternek, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Pu, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Sanders, M., Savary, G., Scherer, S., Scott, G., Shutsman, S., Shen, R., Shetty, D., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smales, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrell, R., Sores, J., Steele, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wlezyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

```

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GFRN
Center clone name: CH230-42A2
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 231272 bases at least Q40
Consensus quality: 234148 bases at least Q30
Consensus quality: 235932 bases at least Q20
Estimated insert size: 240545; sum-of-coverage estimation
Quality coverage: 7x in Q20 bases; sum-of-coverage estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 264609: contig of 264609 bp in length
* 264610 264709: gap of unknown length
* 264710 266632: contig of 1923 bp in length.
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FEATURES
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end sequence: BH345974"
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ORIGIN
Query Match 1.0%; Score 27; DB 2; Length 266632;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2653 CAATTGACAAAAA 2679
DB 247436 CAATTGACAAAAA 247462

RESULT 48
AC115400/c 269117 bp DNA linear HTG 08-OCT-2002
LOCUS Rattus norvegicus clone CH230-59M6, *** SEQUENCING IN PROGRESS ***,
DEFINITION 5 unordered pieces.

```

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ACCESSION
AC115400
AC115400.4 GI:23270024
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 269117)
REFERENCE
AUTHORS
Muzny, D., Maric, M., Melker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooke, S., Amin, A., Angiano, D.,
Angelichech, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Gante, R., Garcia, A., Garner, T., Garza, M.,
Gebregorjis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
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Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
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Wright, D., Wright, R., Wu, J., Yakub, X., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 269117)
Morley, K.C.
Direct Submission
Submitted (19-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 269117)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
On Sep 23, 2002 this sequence version replaced gi:22450411.

```


The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequencing contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNMW
Center clone name: CH230-59M6

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 180274 bases at least Q40
Consensus quality: 183104 bases at least Q30
Consensus quality: 185338 bases at least Q20
Estimated insert size: 198590; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html>).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 86595: contig of 86595 bp in length
* 86596 86695: gap of unknown length
* 86696 167948: contig of 81253 bp in length
* 167949 168048: gap of unknown length
* 168049 265576: contig of 97528 bp in length
* 265577 266793: gap of unknown length
* 266794 266894: contig of 1117 bp in length
* 266894 269117: gap of unknown length
* 269117: contig of 2224 bp in length.

FEATURES

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1. 269117
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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1. 1682
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/note="wgs contig"

ORIGIN

Query Match 1.0%; Score 27; DB 2; Length 269117;
Beet Local Similarity 100.0%; Pred.No.0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2653 CAATTCACAAAAAAAAAAAAAAAAA 2679
Db 42476 CAATTCACAAAAAAAAAAAAAAAAA 42450

RESULT 49
AC131863 322833 bp DNA linear HTG 23-NOV-2002
LOCUS AC131863

DEFINITION

Rattus norvegicus clone CH230-433M17, *** SEQUENCING IN PROGRESS
*** 10 unordered pieces.

ACCESSION

AC131863 GI:25188440

VERSION

HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 322833)

REFERENCE

1 (bases 1 to 322833)

Muzny,D,Marxer,M, Lee, A, Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benham, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Casar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Ditya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Bayes, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebreyes, E., Geer, K., Gill, R., Girdy, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kows, C., Kratt, C.L., Labow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorenshew, L., Louised, H., Lozano, R.J., Lu, X., Ma, J.,

Maheshwari, M., Mahindarne, M., Mahmoud, M., Mallory, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, B.,

Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, B.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Mundaas, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwackelme, O., Okunonu, G., Olampunagun, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Frankoch, C.,

Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,

Sanders, W., Savery, G., Scherer, S., Scott, G., Shattman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajda, D.,

Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, D.,

Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,

Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K.,

Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,

Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,

Williams, G., Willson, R., Wleczek, R., Woodson, H., Woley, K.,

Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von

Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,

Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 322833)

Rat Genome Sequencing Consortium.

Submitted (27-AUG-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 322833)

Rat Genome Sequencing Consortium.

Submitted (23-NOV-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

COMMENT

Baylor Plaza, Houston, TX 77030, USA
 On Nov 23, 2002 this sequence version replaced gi:23322024.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Center: Baylor College of Medicine
 Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVEC
 Center clone name: CH230-433M17

----- Summary Statistics

Assembly program: Phrap; version 0.990329
 Consensus quality: 272635 bases at least Q40
 Consensus quality: 278236 bases at least Q30
 Consensus quality: 281659 bases at least Q20
 Estimated insert size: 275728; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draat_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 14872: contig of 14872 bp in length
* 14873 14972: gap of unknown length
* 14873 46078: gap of 31106 bp in length
* 46079 46178: gap of unknown length
* 46179 51691: contig of 5513 bp in length
* 51692 51791: gap of unknown length
* 51792 113737: contig of 61946 bp in length
* 113738 113837: gap of unknown length
* 113838 313242: contig of 199405 bp in length
* 313243 313342: gap of unknown length
* 313343 314356: contig of 1014 bp in length
* 314357 314456: gap of unknown length
* 314457 316001: contig of 1545 bp in length
* 316002 316101: gap of unknown length
* 316102 317157: contig of 1056 bp in length
* 317158 317257: gap of unknown length
* 317258 318770: contig of 1513 bp in length
* 318771 322833: contig of 3963 bp in length.
* 318871

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FEATURES

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misc_feature 14973..16147
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misc_feature 21483..22546

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ORIGIN

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misc_feature 78005..79490 /note="wgs contig"
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Query Match

Best Local Similarity 1.0%; Score 27; DB 2; Length 322833;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2653 CAATTGACAAAAA 2679

DB 170299 CAATTGACAAAAA 170325

RESULT 50

ATH529544
 LOCUS
 DEFINITION

ACCESSION

ATH529544
 VERSION

KEYWORDS

left border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana (chale crese)

ORGANISM

Arabidopsis thaliana

REFERENCE

1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechold, N., Cnuad, C., Derose, R., Pelletier, G.,
 Lepoint, L., Caboche, M., and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites

AUTHORS

EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE

EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL

EMBO Rep. 3 (12), 1152-1157 (2002)

MEDLINE

2246565

PUBMED

2 (bases 1 to 444)

REFERENCE

Balzerque, S.

AUTHORS

Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue

JOURNAL

Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

FEATURES

Location/Qualifiers

source

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/db_xref="taxon:3702"
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1..444
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left border"
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ORIGIN

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Best Local Similarity 100.0%; Pred.No. 0.021;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2654 AAATTGACAAAAAAAAAAAAAAAAAAAA 2679
          |||||
```

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Db       390 AAATTGACAAAAAAAAAAAAAAAAAAAA 415
          |||||
```

Search completed: January 15, 2005, 10:12:12
Job time : 11210 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 00:57:51 : Search time 1230 Seconds

(without alignments)
11433.495 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagaatcgcgcagcagcgcg.....acaaaaaaaaaaaaaaaaa 2679

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 20

Total number of hits satisfying chosen parameters: 18399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

N_Geneseq_23Sep04:*
1: geneseq1980s:*
2: geneseq1980s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2001s:*
6: geneseq2002s:*
7: geneseq2002s:*
8: geneseq2003s:*
9: geneseq2003s:*
10: geneseq2003s:*
11: geneseq2003s:*
12: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2679	100.0	2679	5 AAF30352	Aaf30352 Human chr
2	2133	79.6	2639	4 AAH14542	Aah14542 Human cDN
3	1995	74.5	1995	5 AAF89709	Aaf89709 Nucleotid
4	1618	60.4	3181	6 AAB59646	Aab59646 Novel hum
5	1465	54.7	3138	4 AAH14556	Aah14556 Human cDN
6	1024	38.2	2259	4 AAH88903	Aah88903 Human pol
7	944	35.2	2448	11 ADM03388	Adm03388 Human cDN
8	765	28.6	1311	4 AAS25843	Aas25843 Human cDN
9	765	28.6	1311	8 ABX73184	Abx73184 Human nov
10	633	23.6	2186	10 ADA52592	Ada52592 Human cod
11	478	17.8	816	4 AAH06828	Aah06828 Human cDN
12	468	17.5	824	4 AAH06846	Aah06846 Human cDN
13	455	17.0	693	4 AAS26304	Aas26304 Human cDN
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15	426	15.9	518	4 AAH11859	Aah11859 Human cDN
16	285	10.7	575	3 AAA44336	Aaa44336 Human sec
17	267	10.0	357	4 AAS26143	Aas26143 Human cDN
18	267	10.0	357	8 ABX73484	Abx73484 Human nov
19	238	8.9	354	4 AAS26563	Aas26563 Human cDN
20	238	8.9	354	4 AAS26144	Aas26144 Human cDN
21	238	8.9	354	8 ABX73904	Abx73904 Human nov

22	238	8.9	354	8	ABX73485	Abx73485 Human nov
23	217	8.1	449	5	ACH26450	Ach26450 Human adu
24	159	6.3	13836	5	ABA16633	AbA16633 Human ner
25	139	5.2	825	4	AAK58374	Aak58374 Human lim
26	78	2.9	617	6	ABN60913	Abn60913 Human can
27	77	2.9	476	9	ACH14968	Ach14968 Human adu
28	60	2.2	60	6	ABN33472	Abn33472 Human spl
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32	25	0.9	1963	6	AAQ39143	Aaq39143 Human tra
33	25	0.9	1963	10	ADD37442	Add37442 Human tra
34	25	0.9	2000	6	ABZ15532	Abz15532 Arabidops
35	25	0.9	2000	8	ADA69051	Ada69051 Arabidops
36	25	0.9	2424	12	ADK67852	Adk67852 Phosphod
37	25	0.9	95769	8	ADK68659	Adk68659 Arabidops
38	24	0.9	199	6	ABL86644	AbL86644 Human ova
39	24	0.9	222	5	AA529141	Aa529141 cDNA enco
40	24	0.9	222	5	AA529069	Aa529069 cDNA enco
41	24	0.9	222	6	AB568281	Ab568281 cDNA enco
42	24	0.9	222	6	AB568209	Ab568209 cDNA enco
43	24	0.9	222	10	ADC25203	Adc25203 Human cDN
44	24	0.9	222	10	ADC25275	Adc25275 Human cDN
45	24	0.9	291	5	ABV20036	Abv20036 Human pro
46	24	0.9	413	5	ABV49795	Abv49795 Human pro
47	24	0.9	525	5	ACH23460	Ach23460 Human adu
48	24	0.9	525	5	ABV60912	Abv60912 Human pro
49	24	0.9	532	8	ACC60485	Acc60485 Rice leaf
50	24	0.9	532	10	ACP56929	Acc56929 Rice leaf
51	24	0.9	703	6	ABQ57317	Abq57317 Human col
52	24	0.9	1486	12	ADN75971	Adn75971 Human sig
53	24	0.9	2003	12	ADP22565	Adp22565 Sea-squir
54	24	0.9	2428	10	AAQ13316	Aaq13316 Human DMS
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56	24	0.9	11869	4	AA536792	Aa536792 Human car
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58	24	0.9	178870	10	ADL13512	Adl13512 Osteoarth
59	24	0.9	349881	10	ADC86642	Adc86642 Human GPC
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61	23	0.9	222	6	AAH87000	Aah87000 Human ova
62	23	0.9	242	4	AAH02577	Aah02577 Human rep
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64	23	0.9	374	6	ABK90577	Abk90577 Human tar
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66	23	0.9	410	4	AAH82951	Aah82951 Human pol
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68	23	0.9	469	9	ACH25805	Ach25805 Human adu
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70	23	0.9	493	9	ACH32353	Ach32353 Human end
71	23	0.9	558	10	ACC55516	Acc55516 Rice endo
72	23	0.9	571	6	ABX09781	Abx09781 M. Incogn
73	23	0.9	592	8	ACC55401	Acc55401 Rice endo
74	23	0.9	601	12	ADQ63420	Adq63420 Transcript
75	23	0.9	636	2	AAQ38312	Aaq38312 ANS 0-13
76	23	0.9	726	4	AAH97185	Aah97185 Human neu
77	23	0.9	752	12	ADN88793	Adn88793 Nicotiana
78	23	0.9	759	6	ABQ55407	Abq55407 Human ova
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81	23	0.9	922	10	ADC86496	Adc86496 Human GPC
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89	23	0.9	1263	3	AAZ50385	Aaz50385 Mouse tes
90	23	0.9	1278	6	ABK61454	Abk61454 Human cDN
91	23	0.9	1347	3	AAZ63330	Aaz63330 cDNA enco
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94	23	0.9				

241	22	0.8	1114	8	ACF20244	Human sec	314	22	0.8	1114	8	ACA65408	Human PRO
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248	22	0.8	1114	8	ACD04816	Novel hum	321	22	0.8	1114	8	ACC92050	Human sec
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250	22	0.8	1114	8	ACD08284	Human sec	323	22	0.8	1114	8	ACA91778	Human PRO
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255	22	0.8	1114	8	ACD15925	Human sec	328	22	0.8	1114	8	ACD16539	Human sec
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258	22	0.8	1114	8	ACC88257	Human sec	331	22	0.8	1114	8	ACA97662	Human PRO
259	22	0.8	1114	8	ACD21611	Human sec	332	22	0.8	1114	9	ACA99111	Novel hum
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263	22	0.8	1114	8	ACD09819	Human sec	336	22	0.8	1114	9	ACC95897	Human sec
264	22	0.8	1114	8	ACC88564	Human sec	337	22	0.8	1114	9	ACF16460	Human sec
265	22	0.8	1114	8	ACD21304	Human sec	338	22	0.8	1114	9	ACF16460	Human sec
266	22	0.8	1114	8	ABX75676	Human CDN	339	22	0.8	1114	9	ACF02578	Human sec
267	22	0.8	1114	8	ABX97879	Human PRO	340	22	0.8	1114	9	ACF02885	Human sec
268	22	0.8	1114	8	ACA97355	Novel hum	341	22	0.8	1114	9	ACF21472	Human sec
269	22	0.8	1114	8	ACA57818	Human PRO	342	22	0.8	1114	9	ACF10156	Human sec
270	22	0.8	1114	8	ACD14346	Human PRO	343	22	0.8	1114	9	ACF78049	Human sec
271	22	0.8	1114	8	ACC91129	Human sec	344	22	0.8	1114	9	ACD46754	Human sec
272	22	0.8	1114	8	ACC88871	Human sec	345	22	0.8	1114	9	ACD49517	Human sec
273	22	0.8	1114	8	ACD07068	Human PRO	346	22	0.8	1114	9	ACF28284	Human sec
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284	22	0.8	1114	8	ACA90992	Novel hum	357	22	0.8	1114	9	ACD31980	Human sec
285	22	0.8	1114	8	ACA70774	Human sec	358	22	0.8	1114	9	ACF18788	Human sec
286	22	0.8	1114	8	ACA95284	Novel hum	359	22	0.8	1114	9	ACF09235	Human sec
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292	22	0.8	1114	8	ACA73213	Novel hum	365	22	0.8	1114	9	ACF50420	Human sec
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295	22	0.8	1114	8	ACA70467	Novel hum	368	22	0.8	1114	9	ACD41623	Human sec
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595	22	0.8	1114	9	ACD10126	ACd10126 Human sec	668	22	0.8	1114	10	ACB87029	ACB87029 Human sec
596	22	0.8	1114	9	ACD16851	ACd16851 cDNA enco	669	22	0.8	1114	10	ACD04202	ACD04202 Human sec
597	22	0.8	1114	9	ACG99148	ACG99148 Human sec	670	22	0.8	1114	10	ACA69533	ACA69533 cDNA enco
598	22	0.8	1114	9	ACF00542	ACf00542 Human sec	671	22	0.8	1114	10	ACA90378	ACA90378 Novel hum
599	22	0.8	1114	9	ACD41009	ACd41009 Human sec	672	22	0.8	1114	10	ACB89485	ACB89485 Human sec
600	22	0.8	1114	9	ACF14618	ACf14618 Human sec	673	22	0.8	1114	10	ACB98276	ACB98276 Novel hum
601	22	0.8	1114	9	ACF22393	ACf22393 Human sec	674	22	0.8	1114	10	ACA93918	ACA93918 Human sec
602	22	0.8	1114	9	ACF78970	ACf78970 Human sec	675	22	0.8	1114	10	ACD15311	ACD15311 Human sec
603	22	0.8	1114	9	ACD67963	ACd67963 Novel hum	676	22	0.8	1114	10	ACD08898	ACD08898 Human sec
604	22	0.8	1114	9	ACF11691	ACf11691 Human sec	677	22	0.8	1114	10	ACG96818	ACG96818 Human sec
605	22	0.8	1114	9	ACF51648	ACf51648 Human sec	678	22	0.8	1114	10	ACF15539	ACf15539 Human sec

679	22	0.8	1114	10	ACA72906	Human	PRO	752	22	0.8	1803	12	ADQ23123	AaQ23123	Human	BOF
680	22	0.8	1114	10	ACD03078	Novel	hum	753	22	0.8	1895	10	ADBS5309	AdB55309	Primary r	
681	22	0.8	1114	10	ACD01893	Novel	hum	c 754	22	0.8	1899	3	AAQ39113	AaQ39113	Arbidiops	
682	22	0.8	1114	10	ACA92085	Novel	hum	c 755	22	0.8	1946	6	ABK35872	AbK35872	CDNA	segu
683	22	0.8	1114	11	ADL32877	Novel	hum	756	22	0.8	1959	2	AAZ77529	AaZ77529	Human	ova
684	22	0.8	1114	11	ADM30411	Novel	hum	757	22	0.8	1979	12	ADQ23884	AdQ23884	Human	bof
685	22	0.8	1114	12	ADE74408	Human	sec	758	22	0.8	1987	6	AB189553	Ab189553	Human	bof
686	22	0.8	1114	12	ADE75020	Human	sec	c 759	22	0.8	1989	3	AAAS1408	AaA51408	Human	pol
687	22	0.8	1114	12	ADE96483	Human	CDN	760	22	0.8	2000	6	AB216968	Ab216968	Arbidiops	
688	22	0.8	1114	12	ADP245794	Human	CDN	c 761	22	0.8	2000	6	AB216205	Ab216205	Arbidiops	
689	22	0.8	1114	12	ADP24593	Human	CDN	762	22	0.8	2000	6	AB217208	Ab217208	Arbidiops	
690	22	0.8	1114	12	ADP29429	Human	CDN	763	22	0.8	2000	6	AB215869	Ab215869	Arbidiops	
691	22	0.8	1114	12	ADP96360	Human	CDN	764	22	0.8	2000	6	AB216212	Ab216212	Arbidiops	
692	22	0.8	1114	12	ADP96233	Novel	hum	765	22	0.8	2173	12	ADQ18866	AdQ18866	Human	bof
693	22	0.8	1114	12	ADG04504	Novel	hum	766	22	0.8	2187	2	AAQ00693	AaQ00693	Human	sec
694	22	0.8	1114	12	ADG00664	Novel	hum	767	22	0.8	2223	2	AAQ00724	AaQ00724	Human	sec
695	22	0.8	1114	12	ADG82920	Human	PRO	768	22	0.8	2256	2	AAQ00722	AaQ00722	Human	sec
696	22	0.8	1114	12	ADH02398	Human	CDN	769	22	0.8	2260	6	ABO54562	AbO54562	Human	ova
697	22	0.8	1114	12	ADH03352	Human	CDN	770	22	0.8	2282	12	ADQ24772	AdQ24772	Human	bof
698	22	0.8	1114	12	ADH03475	Human	CDN	771	22	0.8	2320	10	ADC35627	AdC35627	Rice	SSE1
699	22	0.8	1114	12	ADH26201	Novel	hum	772	22	0.8	2324	3	AAQ59727	AaQ59727	Human	sec
700	22	0.8	1114	12	ADH33170	Human	PRO	773	22	0.8	2339	6	ABT11207	AbT11207	TRC8	rela
701	22	0.8	1114	12	ADH04429	Human	CDN	774	22	0.8	2339	6	ABK10429	AbK10429	Human	PHI
702	22	0.8	1114	12	ADH61430	Human	CDN	775	22	0.8	2366	12	ADK60464	AdK60464	Angiogene	
703	22	0.8	1114	12	ADJ54309	Human	PRO	776	22	0.8	2366	12	ADK60765	AdK60765	Angiogene	
704	22	0.8	1114	12	ADJ64680	Human	PRO	777	22	0.8	2366	12	ADP73087	AdP73087	Angiogene	
705	22	0.8	1114	12	ADM31576	Novel	hum	c 778	22	0.8	2422	2	AAQ11711	AaQ11711	Shuttle v	
706	22	0.8	1114	12	ADM31576	Novel	hum	779	22	0.8	2438	4	AAQ07829	AaQ07829	Human	sec
707	22	0.8	1114	12	ADM36623	Novel	hum	780	22	0.8	2483	3	AAZ33331	AaZ33331	Human	sec
708	22	0.8	1114	12	ADM40428	Novel	hum	781	22	0.8	2505	6	ABT11202	AbT11202	Coding se	
709	22	0.8	1114	12	ADL94629	Human	CDN	782	22	0.8	2505	6	ABK10424	AbK10424	Human	CDN
710	22	0.8	1152	2	AAZ24842	Human	sec	783	22	0.8	2505	6	ABK10424	AbK10424	Human	CDN
711	22	0.8	1173	2	AAZ00358	Human	sec	784	22	0.8	2517	6	ABT11204	AbT11204	RING-SH c	
712	22	0.8	1173	5	AAAF89020	Human	FAT	785	22	0.8	2517	6	ABK10426	AbK10426	Human	TRC
713	22	0.8	1193	3	AAAF59711	Human	sec	786	22	0.8	2532	12	ADQ23253	AdQ23253	Human	bof
714	22	0.8	1201	4	AAAF32780	Human	sec	787	22	0.8	2533	6	AA141419	Aa141419	Maize pro	
715	22	0.8	1266	6	ABK35725	CDNA	segu	788	22	0.8	2547	8	ABX11731	AbX11731	CDNA	enco
716	22	0.8	1287	2	AAV80230	Maize	OTE	789	22	0.8	2608	2	AAQ95541	AaQ95541	Partial A	
717	22	0.8	1298	8	ABZ73441	Human	sec	790	22	0.8	2727	12	ADQ24794	AdQ24794	Human	bof
718	22	0.8	1298	8	ABZ73441	Human	sec	791	22	0.8	2869	5	AA193852	Aa193852	Human	ato
719	22	0.8	1298	8	ADA98004	Human	sec	792	22	0.8	2869	5	AA193852	Aa193852	Human	ato
720	22	0.8	1298	10	ABZ67048	Human	sec	793	22	0.8	2883	3	AAZ90784	AaZ90784	Mouse ner	
721	22	0.8	1311	3	AAZ98307	Human	sec	794	22	0.8	2933	3	AAZ93703	AaZ93703	PRO172 DN	
722	22	0.8	1314	5	AA889578	DNA	enco	795	22	0.8	2933	3	AAZ93703	AaZ93703	PRO172 DN	
723	22	0.8	1314	10	ADK56592	Plant	CDNA	796	22	0.8	2933	3	AAZ93703	AaZ93703	PRO172 DN	
724	22	0.8	1348	10	ADD45618	Human	gen	797	22	0.8	2933	3	AAZ93703	AaZ93703	PRO172 DN	
725	22	0.8	1384	10	ADP28720	Human	NOV	798	22	0.8	2933	3	AAZ93703	AaZ93703	PRO172 DN	
726	22	0.8	1384	12	ADM93465	Human	NOV	799	22	0.8	2933	4	AAZ93703	AaZ93703	PRO172 DN	
727	22	0.8	1387	5	ADM93465	Human	NOV	800	22	0.8	2933	4	AAZ93703	AaZ93703	PRO172 DN	
728	22	0.8	1404	2	AAV32834	Rabbit	lo	801	22	0.8	2933	8	ACN03775	AcN03775	CDNA	enco
729	22	0.8	1404	5	AAH26487	Rabbit	lo	802	22	0.8	2933	8	ACN03775	AcN03775	CDNA	enco
730	22	0.8	1418	10	ADP68448	S. arundi		803	22	0.8	2933	8	ACD41967	AcD41967	Human	sec
731	22	0.8	1422	3	AAAF15991	Human	pro	804	22	0.8	2933	8	ACD41967	AcD41967	Human	sec
732	22	0.8	1474	4	AAAF15991	Human	pro	805	22	0.8	2933	8	ACD41967	AcD41967	Human	sec
733	22	0.8	1474	4	ABK43609	Human	CDN	806	22	0.8	2933	9	ADA45864	AdA45864	Novel	hum
734	22	0.8	1474	6	ABO66546	Human	pol	807	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
735	22	0.8	1474	10	ADP10568	Human	CDN	808	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
736	22	0.8	1474	12	ADP10568	Human	CDN	809	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
737	22	0.8	1486	2	AAAX02855	Human	zbi	810	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
738	22	0.8	1506	12	ADN050591	Antiporci		811	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
739	22	0.8	1540	5	ABAF13110	Human	net	812	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
740	22	0.8	1557	3	AAZ49567	Maize	MIO	813	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
741	22	0.8	1592	6	AB158954	Human	tum	814	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
742	22	0.8	1597	10	ADP28722	Human	NOV	815	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
743	22	0.8	1597	12	ADM93467	Human	NOV	816	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
744	22	0.8	1606	6	AB190102	Human	pol	817	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
745	22	0.8	1619	3	AAAF4283	Human	mes	818	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
746	22	0.8	1641	9	ADAF11580	Human	CDN	819	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
747	22	0.8	1720	3	AAAC0008	Human	sec	820	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
748	22	0.8	1722	5	AAAD06860	Human	bte	821	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
749	22	0.8	1732	12	ADP22631	Sea-squid		822	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
750	22	0.8	1745	12	ADN89497	Human	PIA	823	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO
751	22	0.8	1768	4	AAAF5086	Human	col	824	22	0.8	2933	9	ADA76295	AdA76295	Human	PRO

XX Novel nucleic acid sequence of mitotic checkpoint gene encoding a
PT checkpoint with forkhead-associated domain and ring finger protein, for
PT diagnosing tumorigenic cells and in screening for anticancer drugs.
XX
XX
XX Claim 2 (a); Fig 4A-D; 85bp; English.
XX
XX The present sequence is that of cDNA encoding the human mitotic
CC checkpoint protein Chfr (see AAB20219) having a forkhead associated
CC domain (FHA) and a ring finger domain. The protein is required for
CC regulation of the transition of cells from prophase to metaphase during
CC mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint
CC was evident in primary human cells, but was inactivated in 4 of 8 human
CC cancer cell lines. In U2OS cells, a mutation was identified, which caused
CC a Val to Met amino acid substitution in the highly conserved C-terminal
CC Cys-rich region of the Chfr protein. In the absence of the Chfr
CC checkpoint, cells subjected to mitotic stress condensed their chromosomes
CC despite failing to separate their chromosomes. Chfr may monitor
CC centrosome separation. Inactivation of the Chfr gene in human cancer is
CC theorized to underlie the increased sensitivity of cancer cells to
CC antimitotic drugs. Nucleic acids comprising the present sequence, or
CC sequences encoding at least amino acids 31-103, 303-346, 476-641 (or
CC their antisense sequences) are claimed. The Chfr cDNA was isolated from
CC an expressed sequence tag database sequence for cDNAs with FHA motifs.
CC Claimed methods of determining the tumorigenic potential of a cell
CC comprise examining the cell for the presence of Chfr nucleic acid
CC (absence or mutation indicating predisposition to tumorigenesis upon
CC exposure to mitotic stress). Also claimed is a diagnostic agent, e.g. an
CC antisense fragment of the present sequence, that binds to the Chfr
CC nucleic acid, and a diagnostic kit for detecting tumorigenic potential

11

CC XX SQ	sensitive to additional antitumour therapies
Sequence 2679 BP; 650 A; 715 C; 764 G; 550 T; 0 U; 0 Other;	

Matches 2679; Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 1 AAGATTGGCAGGCGCATGTCTTGACAGCGCGCGCGGTTCCGG 60

Db 1 AAGAA TTCG GCA CGAG GCG CGCA ATG CTC TTG A CAC GCG CGCG CGG CAG CGG GTT CCG G 60

Qy 61 GTT GCG CGCG CGG GCG CGG GAT GTG AAT CCC GAT GGA CCG GCG CCG GAG AAG CAA GCA TCG 120

db 61 GTTCGGCGCGGCGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGCAAGCACTCG 120

121 CCGCCGCGAGCCCTGGGACGGCTCTGCCCTCTGGCGCGGAGGGCGAGCCGCAC 180

Db 181 GTCTCTTGAGGAGCGGAGTGAACCATCGGGCGGAGACGAGGTTGCCACTTTCCTTC 240

241 CCCAGCAATAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAATAATCAGGT 300

Db 241 CCCAGCAATAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGATGAATAATCAGGT 300

301 CAGGTGACACTGGAAGATACCAAGCAGTGGACAGTGATTACAAGCTGAAGTTGTT 360

Db 301 CAGGTGACACTGGAAGATACCGACCACTGGACAGTGATTACCAAGCTGAAGTTGTT 360

361 AAGAGCAGACATGCCCTTACAGACTGGGATGTCATCTTGGTGTACAGGAAGAT 420

Db 361 AAGAAGCAGACATGCCCTTACAGACTGGGATGTCATCTACTTGGTGTACAGGAAGAAT 420

421 GAACCGAACACACGTGCATACCTCTATGAATCTTTAAGTGAAAGAAGGCATGACA 480

Db 421 GAACGGAGCAACAAGTGGATACCTGTATGATCTTTAAGTGAAGCAAGGATGACA 480
Qy 481 CAAAGATCTTTTAAAGTAAACAAGAAATGTGTTCATAGGAGCAAAAGTACTTCAGGT 540
Db 481 CAAAGATCTTTTAAAGTAAACAAGAAATGTGTTCATAGGAGCAAAAGTACTTCAGGT 540
Qy 541 GCAGGTGACAGGGGAGGGGCGGATCCCGGGTCCCTCGTGTGAGCCGCACTCAGGTG 600
Db 541 GCAGGTGACAGGGGAGGGGCGGATCCCGGGTCCCTCGTGTGAGCCGCACTCAGGTG 600
Qy 601 TGTCTTGAAGAACCAACAGCCATCAACATGACGTCAGACCTCTTCCCAAGCCTGGCC 660
Db 601 TGTCTTGAAGAACCAACAGCCATCAACATGACGTCAGACCTCTTCCCAAGCCTGGCC 660
Qy 661 TCTTCAACGAGGCTTCTCTGCAAGGGGAGAGGTTCTTCAGTTTGGGTCTGGGGGT 720
Db 661 TCTTCAACGAGGCTTCTCTGCAAGGGGAGAGGTTCTTCAGTTTGGGTCTGGGGGT 720
Qy 721 GGTGGATCTCCCTTAAAGAAAGTGTCTCTGTGGCAAGTGAAGTCTCAGCTT 780
Db 721 GGTGGATCTCCCTTAAAGAAAGTGTCTCTGTGGCAAGTGAAGTCTCAGCTT 780
Qy 781 GCTCAGCTCTCCCAAGCAAGAAAGTGTCTCTGTGGCAAGTGAAGTCTCAGCTT 840
Db 781 GCTCAGCTCTCCCAAGCAAGAAAGTGTCTCTGTGGCAAGTGAAGTCTCAGCTT 840
Qy 841 GAGGATTTGAGGCGCGTGAAGAAAGAAATGAGAGAGATGGGACCTTGAACCTGGG 900
Db 841 GAGGATTTGAGGCGCGTGAAGAAAGAAATGAGAGAGATGGGACCTTGAACCTGGG 900
Qy 901 CAGTTTGGTCCGACACACCGCGTGAAGAAATGCGCAACCGTCCACGAGGAGCTCAGAGCA 960
Db 901 CAGTTTGGTCCGACACACCGCGTGAAGAAATGCGCAACCGTCCACGAGGAGCTCAGAGCA 960
Qy 961 GCGGCTGGGAGGCGCAAGATGAGAGAGAGCGCTGACATGATCATCTGCAAGACTG 1020
Db 961 GCGGCTGGGAGGCGCAAGATGAGAGAGAGCGCTGACATGATCATCTGCAAGACTG 1020
Qy 1021 CTGCAAGACTGCTGTGATTTGCAAGCCCTGTGATGACACGTTCTGCGCGGCTTCTACTCG 1080
Db 1021 CTGCAAGACTGCTGTGATTTGCAAGCCCTGTGATGACACGTTCTGCGCGGCTTCTACTCG 1080
Qy 1081 GGTGTGATGAGGCTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT 1140
Db 1081 GGTGTGATGAGGCTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT 1140
Qy 1141 AAAAAACACATCTCTCAACAACTCTGTGAGACATCTCTATCCAGATCCAGACAGAGT 1200
Db 1141 AAAAAACACATCTCTCAACAACTCTGTGAGACATCTCTATCCAGATCCAGACAGAGT 1200
Qy 1201 CCGAGTGAAGAAATGTGCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 CCGAGTGAAGAAATGTGCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 1260
Qy 1261 CAGCCCAAAAGTCAAGGCGGTCTTTTCTGATGAAGAGGAGTCAAGGAGCTGTGGAG 1320
Db 1261 CAGCCCAAAAGTCAAGGCGGTCTTTTCTGATGAAGAGGAGTCAAGGAGCTGTGGAG 1320
Qy 1321 CTGTGACAGCTTGAAGATGATCTGACATTTAGCCAGCATATGCTGTGTGCTGGAG 1380
Db 1321 CTGTGACAGCTTGAAGATGATCTGACATTTAGCCAGCATATGCTGTGTGCTGGAG 1380
Qy 1381 TGTCTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
Db 1381 TGTCTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
Qy 1441 CCAAGAGCCCAAGAGGCGCTGTGGGAGTGAACCTTCAAGCTCGTCAAGCTGAGAGCA 1500
Db 1441 CCAAGAGCCCAAGAGGCGCTGTGGGAGTGAACCTTCAAGCTCGTCAAGCTGAGAGCA 1500
Qy 1501 GTTCAAGATTAAGTGTGCTCTGCAAGAGAGCAAGCTGTGACCTGTGCTTCCAG 1560
Db 1501 GTTCAAGATTAAGTGTGCTCTGCAAGAGAGCAAGCTGTGACCTGTGCTTCCAG 1560

Qy 1561 CCAATGCCCGA CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
Db 1561 CCAATGCCCGA CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
Qy 1621 GCGGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Db 1621 GCGGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Qy 1681 GGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Db 1681 GGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Qy 1741 AACAACAAGCTACAGAGTGAACATCTGGAAGAAATTAAGTGAAGAAATTAAGTGAAGAA 1800
Db 1741 AACAACAAGCTACAGAGTGAACATCTGGAAGAAATTAAGTGAAGAAATTAAGTGAAGAA 1800
Qy 1801 TGAAGAAACATGTTGACCGAGAGCTGTGAGCTCTCAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 TGAAGAAACATGTTGACCGAGAGCTGTGAGCTCTCAGGAGGAGGAGGAGGAGGAGGAG 1860
Qy 1861 GATTACAGAGTCAAGGAGAGCACCGTTCTGTGTTACTGTGTGAGCTGTGAGCTGTGAG 1920
Db 1861 GATTACAGAGTCAAGGAGAGCACCGTTCTGTGTTACTGTGTGAGCTGTGAGCTGTGAG 1920
Qy 1921 GAGTGAACCTATCAGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Db 1921 GAGTGAACCTATCAGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Qy 1981 TCCGCTCTGACCTGCTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db 1981 TCCGCTCTGACCTGCTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Qy 2041 ATGAATTCATATCATATCTGTGAAGACAGCAAGGTTCAAAATTAAGATTCAGAGGCTT 2100
Db 2041 ATGAATTCATATCATATCTGTGAAGACAGCAAGGTTCAAAATTAAGATTCAGAGGCTT 2100
Qy 2101 GAGGAGCTTTCAGACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
Db 2101 GAGGAGCTTTCAGACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
Qy 2161 TCAAGGTTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
Db 2161 TCAAGGTTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
Qy 2221 GGTGACTTTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Db 2221 GGTGACTTTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Qy 2281 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
Db 2281 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
Qy 2341 CGAAGGCTTTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
Db 2341 CGAAGGCTTTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
Qy 2401 ATTTTCGAAACTCAAGTTAAAGCAGAGTCTGTGTTTCAAGAAAGTTTCAAGGAGAGG 2460
Db 2401 ATTTTCGAAACTCAAGTTAAAGCAGAGTCTGTGTTTCAAGAAAGTTTCAAGGAGAGG 2460
Qy 2461 GGTGAATTTATCAAAAACATGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Db 2461 GGTGAATTTATCAAAAACATGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Qy 2521 CGTACCAATATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
Db 2521 CGTACCAATATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
Qy 2581 GGTGAGCTTATCTTCTAATTAAGATTTAAATGTCACAACTGTGACCAATTAATTA 2640
Db 2581 GGTGAGCTTATCTTCTAATTAAGATTTAAATGTCACAACTGTGACCAATTAATTA 2640

QY 2641 ATTATATATTACAAATTCACAAAAA 2679
DB 2641 ATTATATATTACAAATTCACAAAAA 2679

RESULT 2
AAH14542
ID AAH14542 standard; cDNA; 2639 BP.

XX AAH14542;
XX
XX 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:12099.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX BP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INSR.

XX Oca T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR MPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX Claim 8; SEQ ID NO 12099; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primer sets are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX Sequence 2639 BP; 620 A; 706 C; 760 G; 553 T; 0 U; 0 Other;

Query Match 79.6%; Score 2133; DB 4; Length 2639;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 GATACCTCAGGTGACAGTGCAGAGGCGAGCCGATCCCGGGTCCCTCCGTGCGCC 588
DB 481 GATACCTCAGGTGACAGTGCAGAGGCGAGCCGATCCCGGGTCCCTCCGTGCGCC 540
QY 589 GCCACTCAGGTGTGCTTTGAGGAATCCAGCCATCAATCGAGCTCAGACTCTTTCC 648
DB 541 GCCACTCAGGTGTGCTTTGAGGAATCCAGCCATCAATCGAGCTCAGACTCTTTCC 600
QY 649 ACAGCTCGGCTCTTCCAGGAGCTTCTCCGAGGCGAGAGCTTCTCCAGTTGT 708
DB 601 ACAGCTCGGCTCTTCCAGGAGCTTCTCCGAGGCGAGAGCTTCTCCAGTTGT 660
QY 709 GGGTCTGGGGGTGTGGCATCTCCCTAAAGAAATGATGCTCTGTGGCAATGATGA 768
DB 661 GGGTCTGGGGGTGTGGCATCTCCCTAAAGAAATGATGCTCTGTGGCAATGATGA 720
QY 769 GTCTCCAGCTTTGCTCAGCTCTCCCAAGAAAGATCTGCTTTTGTCTTGGAA 828
DB 721 GTCTCCAGCTTTGCTCAGCTCTCCCAAGAAAGATCTGCTTTTGTCTTGGAA 780
QY 829 CCCAGATCAGAGAGATTTGAGAGCCGCTGAAGAAATGAGAGATGAGGACCTT 888
DB 761 CCCAGATCAGAGAGATTTGAGAGCCGCTGAAGAAATGAGAGATGAGGACCTT 840
QY 889 GACTTGAACGGGAGTTGTGTGTGACACACCGCTGAGAAATGCCCAACCGTCCAGAG 948
DB 841 GACTTGAACGGGAGTTGTGTGTGACACACCGCTGAGAAATGCCCAACCGTCCAGAG 900
QY 949 GACGTCAAGAGCAGCGCGTGGAGAGCAGAAATGAGAGAGAGCCTGACATGATCATC 1008
DB 901 GACGTCAAGAGCAGCGCGTGGAGAGCAGAAATGAGAGAGAGCCTGACATGATCATC 960
QY 1009 TCCAGAGACTCTGTCAGACAGTGCCTGATTTGACAGCCCTGATGACACAGTTCCGCG 1068
DB 961 TCCAGAGACTCTGTCAGACAGTGCCTGATTTGACAGCCCTGATGACACAGTTCCGCG 1020
QY 1069 GTTGTCTCTCTGGGTGTGATGAGCGCTGTCTGTCTCTGCTGCTGCTGCTGCTG 1128
DB 1021 GTTGTCTCTCTGGGTGTGATGAGCGCTGTCTGTCTCTGCTGCTGCTGCTGCTG 1080
QY 1129 GAGCGGATCTGTAAACCAATCCTCAACACCTCGGAGAGCATCTCATTCAGCAT 1188
DB 1081 GAGCGGATCTGTAAACCAATCCTCAACACCTCGGAGAGCATCTCATTCAGCAT 1140
QY 1189 CCAGCAAGAGTGCAGTGAAGAAATGTGCAAAATATGATGCCAGGATTAATCACT 1248
DB 1141 CCAGCAAGAGTGCAGTGAAGAAATGTGCAAAATATGATGCCAGGATTAATCACT 1200
QY 1249 CAAGCATGCTGCAGCCCAAGTCAAGGCGTCTTTTCTGATGAAGAGAGTTCAGAG 1308
DB 1201 CAAGCATGCTGCAGCCCAAGTCAAGGCGTCTTTTCTGATGAAGAGAGTTCAGAG 1260
QY 1309 GACCTGTGAGCTGTGAGAGTGTGACAGTGTCTGACATTAAGCCATTAACGTC 1368
DB 1261 GACCTGTGAGCTGTGAGAGTGTGACAGTGTCTGACATTAAGCCATTAACGTC 1320
QY 1369 GTGTGCGGCAATGTCTGAGTACAGAAAGCAGCGCGCAGCTTCCCACTGCCAGCA 1428
DB 1321 GTGTGCGGCAATGTCTGAGTACAGAAAGCAGCGCGCAGCTTCCCACTGCCAGCA 1380
QY 1429 CCCAGAGGCGAGGAGGAGCCCAAGGCGCTGGGGAGATGACCTTCCAGTCCGTGAC 1488
DB 1381 CCCAGAGGCGAGGAGGAGCCCAAGGCGCTGGGGAGATGACCTTCCAGTCCGTGAC 1440
QY 1489 CTGACGACAGAGTCCAGATTAAGTGTGCTCTGCAAGAGAACCGCTGTGACAC 1548
DB 1441 CTGACGACAGAGTCCAGATTAAGTGTGCTCTGCAAGAGAACCGCTGTGACAC 1500
QY 1549 TGTGCTTCCAGCCCATGCGGACCGAGAGCGGAGCGGAGCAGACCCCGTGTGCGCC 1608
DB 1501 TGTGCTTCCAGCCCATGCGGACCGAGAGCGGAGCGGAGCAGACCCCGTGTGCGCC 1560

Oy	1609	CCTCAGCAGTGTGGCGGTCTGCCTCGACGCTTTCGCAACCTGTACCTGGAGGCTGCACCCGG	
Dp	1561	CCTCAGCAGTGTGGCGGTCTGCCTCGACGCTTTCGCAACCTGTACCTGGAGGCTGCACCCGG	1620
Oy	1669	ACCGGCTGCTACGCGTGCCTGGCCCCCGTTTTGTGAGCTCAACTGGGTGACAAAGTGTCTG	1728
Dp	1621	ACCGGCTGCTACGCGTGCCTGGCCCCCGTTTTGTGAGCTCAACTGGGTGACAAAGTGTCTG	1680
Oy	1729	GACCGCGGTGCTGAACAACAACAGCTACAGATCCAGAAATTAACCTGGCAAC	1788
Dp	1661	GACCGCGGTGCTGAACAACAACAGCTACAGATCCAGAAATTAACCTGGCAAC	1740
Oy	1789	AGAGTTTGAACATGGAACAAACATGTTGACCGGAGGCTCGTGCTCTCCAGCGGGAGTGTG	1848
Dp	1741	AGAGTTTGAACATGGAACAAACATGTTGACCGGAGGCTCGTGCTCTCCAGCGGGAGTGTG	1800
Oy	1849	TTTCTGCTGTCTGATTTACAGAGTCAAGGAGACACCGTTCTGTGTTACTGCTGTGGCTGTG	1908
Dp	1801	TTTCTGCTGTCTGATTTACAGAGTCAAGGAGACACCGTTCTGTGTTACTGCTGTGGCTGTG	1860
Oy	1909	CGCAGCTTCCGTAAGCTGACCTATCAGTATCGGCGAACAATTCCTGCTCTCCGAGTTGGCA	1968
Dp	1861	CGCAGCTTCCGTAAGCTGACCTATCAGTATCGGCGAACAATTCCTGCTCTCCGAGTTGGCA	1920
Oy	1969	GTCGCGGTAAACATCCCGTCTGTGACTGTAGGGGCGTAACTGCGGACTCAGGTGAAA	2028
Dp	1921	GTCGCGGTAAACATCCCGTCTGTGACTGTAGGGGCGTAACTGCGGACTCAGGTGAAA	1980
Oy	2029	GCTCACCACCGCANTGAATTTCAATCATATCTGTGAACAACAAGTTTCAAAAATTAAACA	2088
Dp	1981	GCTCACCACCGCANTGAATTTCAATCATATCTGTGAACAACAAGTTTCAAAAATTAAACA	2040
Oy	2089	TCCAGAGGCGCTGAGCAGCTTTCAGCACTGAGAGGTGAAGAAGCGTGTTTTAAATACA	2148
Dp	2041	TCCAGAGGCGCTGAGCAGCTTTCAGCACTGAGAGGTGAAGAAGCGTGTGTTTTAAATACA	2100
Oy	2149	GAGACAGACAGTCAAGGTGTTTTCAACGCCCCCTGAGGGAAGGAGCCGAGGGTCTCCGA	2208
Dp	2101	GAGACAGACAGTCAAGGTGTTTTCAACGCCCCCTGAGGGAAGGAGCCGAGGGTCTCCGA	2160
Oy	2209	CAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTACCTGTGAGTGAACCCCTCCCA	2268
Dp	2161	CAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTACCTGTGAGTGAACCCCTCCCA	2220
Oy	2269	GAGCCCCGGGGGCGCAGCCCGCCTCTGTGTAGCGGTGGGCAAGGGCTGTGGTGGCAT	2328
Dp	2221	GAGCCCCGGGGGCGCAGCCCGCCTCTGTGTAGCGGTGGGCAAGGGCTGTGGTGGCAT	2280
Oy	2329	CAGCAGCAGACAGCAAGCTTTCGTGAACATGCGGCGCTCCCGCGAAGGGGCAAGTTT	2388
Dp	2281	CAGCAGCAGACAGCAAGCTTTCGTGAACATGCGGCGCTCCCGCGAAGGGGCAAGTTT	2340
Oy	2389	GCTCTTTGTACATTTTCCGAAACTACAGTTAAAGCAAAAGTCTGTTTCAGGAAAAGTT	2448
Dp	2341	GCTCTTTGTACATTTTCCGAAACTACAGTTAAAGCAAAAGTCTGTTTCAGGAAAAGTT	2400
Oy	2449	TCAAGGAGGAAGGCGAAGTTTACAAAAACATTTTCAAGAGGAAGGACATTAAGTTTA	2508
Dp	2401	TCAAGGAGGAAGGCGAAGTTTACAAAAACATTTTCAAGAGGAAGGACATTAAGTTTA	2460
Oy	2509	CAGCCTACAGGACGTACCAATATCTGTGTGGGAAAACAACAGCATTTTATCTATTT	2568
Dp	2461	CAGCCTACAGGACGTACCAATATCTGTGTGGGAAAACAACAGCATTTTATCTATTT	2520
Oy	2569	TTTATTTTAAATAGTGTGGTGTATCTTCTATTAAGAATTTAAATGTCAAACTGTAGC	2628
Dp	2521	TTTATTTTAAATAGTGTGGTGTATCTTCTATTAAGAATTTAAATGTCAAACTGTAGC	2580
Oy	2629	ACAAATATATTAATTTATTAATTTAAATTAAGC 2661	
Dp	2581	ACAAATATATTAATTTATTAATTTAAATTAAGC 2613	

Result 3	
AAF89709	
ID	AAF89709 standard; DNA; 1995 BP.
XX	
AC	AAF89709;
XX	
DT	22-AUG-2001 (first entry)
XX	
DE	Nucleotide sequence of a human ring finger protein designated FHAR1.
XX	
KW	FHAR1; RING finger protein; cancer; vaccine; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	1..1995
CDS	/*tag= a
FT	/product= "ring finger protein FHAR1"
XX	
FN	WO200142430-A1.
PD	14-JUN-2001.
XX	
PF	07-DEC-2000; 2000MO-US033094.
XX	
PR	08-DEC-1999; 99US-00456876.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Zhou B, Zhu Y, Chaturvedi P, Hurle MR, Li X;
DR	WPI; 2001-381663/40.
XX	P-PsDB; AAB83843.
PT	New FHAR1 polypeptide, a member of the RING finger protein family for
XX	diagnosing and treating cancer, and for use in anti-cancer vaccines.
PS	Claim 2; Page 18-19; 28pp; English.
XX	
CC	The present sequence encodes a FHAR1 polypeptide, which is a member of
CC	the RING finger protein family. FHAR1 is useful in the treatment of
CC	cancer, and as a vaccine for inducing an immunological response in a
CC	mammal. FHAR1 polynucleotides may also be used as a diagnostic reagent
CC	through detection of mutations in the associated gene, and for chromosome
CC	localization studies, and tissue expression studies. FHAR1 antibodies are
CC	useful to isolate and to identify clones expressing the polypeptides, or
CC	to purify the polypeptides by affinity chromatography and to treat cancer
SQ	Sequence 1995 BP; 465 A; 563 C; 580 G; 387 T; 0 U; 0 Other;
Query Match	74.5%; Score 1995; DB 5; Length 1995;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1995; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	91 ATGAGCGGCCGGAGAAGGCAAGCAGTCGCCGCCGCCGCAGCCCTTGCGGACGCGTCTGTG DB 1 ATGAGCGGCCGGAGAAGGCAAGCAGTCGCCGCCGCCGCAGCCCTTGCGGACGCGTCTGTG 60
QY	151 CGTCTGGCGCGGAGAGAGGCGGACGCGCACGTCCTCTTGAGGAACCGGAGATGACCATC 210
DB	61 CGTCTGGCGCGGAGAGAGGCGGACGCGCACGTCCTCTTGAGGAACCGGAGATGACCATC 120
QY	211 GGGCGGAGACGAGGTGTGCGACTTTCTTCCCGACAAATAAAGTGTCTGTGGAATCAGC 270
DB	121 GGGCGGAGACGAGGTGTGCGACTTTCTTCCCGACAAATAAAGTGTCTGTGGAATCAGC 180
QY	271 TGTAAGATTGTAGTGATGAAAATAATCAGGTCAAGTGTGACATGGAAGATACCAGACCAAGT 330
DB	181 TGTAAGATTGTAGTGATGAAAATAATCAGGTCAAGTGTGACATGGAAGATACCAGACCAAGT 240
QY	331 GGAACAGTGATTAACAAGCTGAAGTGTGTAAAGACGACATGCGCCCTTTACAGACTGGG 390
DB	241 GGAACAGTGATTAACAAGCTGAAGTGTGTAAAGACGACATGCGCCCTTTACAGACTGGG 300

QY	391	GATGTCATCTA	CTTGSTGTA	CGAAAGAT	TGAACCGGAA	CAACA	GGTGGCA	TACCT	AT	450					
Db	301	GATGTCATCTA	CTTGSTGTA	CGAAAGAT	TGAACCGGAA	CAACA	GGTGGCA	TACCT	AT	360					
QY	451	GAATCTTTA	AGTGA	AAGCAG	GCATG	ACA	CAAGA	TCTTT	GAAGCTTAA	CAAGAAAT	510				
Db	361	GAATCTTTA	AGTGA	AAGCAG	GCATG	ACA	CAAGA	TCTTT	GAAGCTTAA	CAAGAAAT	420				
QY	511	GTGTTCC	ANTGGGA	CCAAAGAT	ACCTCA	GGTGTGA	GGGGCG	AGGGGG	CCGAT	CCCCGG	570				
Db	421	GTGTTCC	ANTGGGA	CCAAAGAT	ACCTCA	GGTGTGA	GGGGCG	AGGGGG	CCGAT	CCCCGG	480				
QY	571	GTCCCTCCG	TCCGTCCG	CCGCACT	CACTG	AGGTGTCTTT	TGA	GAACA	CAAGGCAT	CAATCG	630				
Db	481	GTCCCTCCG	TCCGTCCG	CCGCACT	CACTG	AGGTGTCTTT	TGA	GAACA	CAAGGCAT	CAATCG	540				
QY	631	ACGTCA	AGACCTT	TCTCCCA	CAGCCT	GTGACCTT	TCC	ACG	AGAGCCTT	CTTCC	AGAGCGGA	690			
Db	541	ACGTCA	AGACCTT	TCTCCCA	CAGCCT	GTGACCTT	TCC	ACG	AGAGCCTT	CTTCC	AGAGCGGA	600			
QY	691	GAGCGT	CCCTCC	AGTTTGG	GGGTCT	GTGGGGGT	TGGTGA	CTCC	CCCTTAA	AGAAAT	GGTGTCC	750			
Db	601	GAGCGT	CCCTCC	AGTTTGG	GGGTCT	GTGGGGGT	TGGTGA	CTCC	CCCTTAA	AGAAAT	GGTGTCC	660			
QY	751	TCTGTGG	CAAGTGA	TGAATCT	TC	CAGCTTTG	CACT	CTTCC	ACA	GAAAGA	CTGCG	810			
Db	661	TCTGTGG	CAAGTGA	TGAATCT	TC	CAGCTTTG	CACT	CTTCC	ACA	GAAAGA	CTGCG	720			
QY	811	TCCCTTT	CGTGGTGA	AACCCAG	ATCA	GGAGATTT	TGA	AGCCCGT	TA	AGAAAGAA	TATG	870			
Db	721	TCCCTTT	CGTGGTGA	AACCCAG	ATCA	GGAGATTT	TGA	AGCCCGT	TA	AGAAAGAA	TATG	780			
QY	871	AGAGAGAT	TGGGGA	CTTGA	CTCTGA	ACGGG	CAGTTGTT	GTGTG	CA	CAACCGCGT	AGAAAT	930			
Db	781	AGAGAGAT	TGGGGA	CTTGA	CTCTGA	ACGGG	CAGTTGTT	GTGTG	CA	CAACCGCGT	AGAAAT	840			
QY	931	GCCCAA	CCGTCC	ACAGAGA	CGTCA	AGACG	CGCTGG	AGAC	CCACA	CAAGATG	AGAGAG	990			
Db	841	GCCCAA	CCGTCC	ACAGAGA	CGTCA	AGACG	CGCTGG	AGAC	CCACA	CAAGATG	AGAGAG	900			
QY	991	ACCGTGA	CATG	CATCTG	CGCAG	AGACCTG	CGTGA	CA	CTGGTGA	GTG	AGGCGCTG	105			
Db	901	ACCGTGA	CATG	CATCTG	CGCAG	AGACCTG	CGTGA	CA	CTGGTGA	GTG	AGGCGCTG	960			
QY	1051	ATGCA	CACGTTCT	GCGCGG	CTTGCTA	CTCGGG	CTGGAAT	GAA	CGCTGT	CCCTGT	GTCTCT	1110			
Db	961	ATGCA	CACGTTCT	GCGCGG	CTTGCTA	CTCGGG	CTGGAAT	GAA	CGCTGT	CCCTGT	GTCTCT	1020			
QY	1111	ACCGCG	CGCTGT	CCGCGTGA	GGGATCT	GTGTAA	AA	CA	CTCTTCA	AA	CACTCGT	GGAA	1170		
Db	1021	ACCGCG	CGCTGT	CCGCGTGA	GGGATCT	GTGTAA	AA	CA	CTCTTCA	AA	CACTCGT	GGAA	1080		
QY	1171	GCATAC	CTCATC	ACACATC	ACAGACA	AGAGT	CGCA	TGGA	AAAGAT	GTCA	AAAGT	TGAT	1230		
Db	1081	GCATAC	CTCATC	ACACATC	ACAGACA	AGAGT	CGCA	TGGA	AAAGAT	GTCA	AAAGT	TGAT	1140		
QY	1231	GCCAGGA	TAAATAT	CACTC	ACAGAC	TGCTG	CAGC	CCCAA	ATG	CAGGCG	CTTTT	CTGAT	1290		
Db	1141	GCCAGGA	TAAATAT	CACTC	ACAGAC	TGCTG	CAGC	CCCAA	ATG	CAGGCG	CTTTT	CTGAT	1200		
QY	1291	GAA	GAGAGGA	AGTTCA	GAGAG	ACCTGT	GTGAG	CGTGA	CA	GTTGA	CAGTGA	GGTCC	CAAC	1350	
Db	1201	GAA	GAGAGGA	AGTTCA	GAGAG	ACCTGT	GTGAG	CGTGA	CA	GTTGA	CAGTGA	GGTCC	CAAC	1260	
QY	1351	ATTAG	CCAGC	CAATAGT	CGTGTG	CGCGG	CAGTGT	CTCTGA	GTAC	AGAGG	CAAGG	CGCGG	CAG	1410	
Db	1261	ATTAG	CCAGC	CAATAGT	CGTGTG	CGCGG	CAGTGT	CTCTGA	GTAC	AGAGG	CAAGG	CGCGG	CAG	1320	
QY	1411	CCTCC	CACTG	CGCCAG	CA	CCGAGGG	CGAG	CGCCACA	AGC	CCCA	AGC	CCCTTGG	GGAGAT	GA	1470
Db	1321	CCTCC	CACTG	CGCCAG	CA	CCGAGGG	CGAG	CGCCACA	AGC	CCCA	AGC	CCCTTGG	GGAGAT	GA	1380

QY	1471	CCCTCCAGCTCCGTCAGAGCTTACACAGACAGAGTCCAGAGTTACAGTGTGCCCTCTGCAAGGA	1530
Db	1381	CCCTCCAGCTCCGTCAGAGCTTACACAGACAGAGTCCAGAGTTACAGTGTGCCCTCTGCAAGGA	1440
QY	1511	AGCCACGCGCTGTGTGACCTGCTGTTCACGCCCATGCCCCGACCGGAGAGCGGACCGCGAG	1590
Db	1441	AGCCACGCGCTGTGTGACCTGCTGTTCACGCCCATGCCCCGACCGGAGAGCGGACCGCGAG	1500
QY	1591	CAGGACCCGCGGTGTGTGCGCCCTCAGACAGTGTGGGTCTGCGCTGAGACCTTTCTGCACTG	1650
Db	1501	CAGGACCCGCGGTGTGTGCGCCCTCAGACAGTGTGGGTCTGCGCTGAGACCTTTCTGCACTG	1560
QY	1651	TACTGGGGCTGTACCCCGGACCGGAGCTGTACCGGCTGCGCTGCGCTTTTGTGAGCTCAAC	1710
Db	1561	TACTGGGGCTGTACCCCGGACCGGAGCTGTACCGGCTGCGCTGCGCTTTTGTGAGCTCAAC	1620
QY	1711	CTGGGTGACAAAGTGTGTGAGAGCGGTGTGTAAACAACAACAGTCAAGTCAAGATCTGT	1770
Db	1621	CTGGGTGACAAAGTGTGTGAGAGCGGTGTGTAAACAACAACAGTCAAGTCAAGATCTGT	1680
QY	1771	AAGAAATTACCTGTGGCAACACAGAGTGTGACATGTGAAAAACATGTGTGACCGAGAGCTGTG	1830
Db	1681	AAGAAATTACCTGTGGCAACACAGAGTGTGACATGTGAAAAACATGTGTGACCGAGAGCTGTG	1740
QY	1831	GCTCTCCAGCGGGAGTGTGTCTGTCTGTCTGTATTAACAAGTCAAGGACAGGACACCGTTCTG	1890
Db	1741	GCTCTCCAGCGGGAGTGTGTCTGTCTGTCTGTATTAACAAGTCAAGGACAGGACACCGTTCTG	1800
QY	1891	TGTTACTGCTGTGTGGCTGTGGCAGGCTTCGAGAGCTGACCTATCAAGTATCCGACAGAACTT	1950
Db	1801	TGTTACTGCTGTGTGGCTGTGGCAGGCTTCGAGAGCTGACCTATCAAGTATCCGACAGAACTT	1860
QY	1951	CCTGCTTCCGAGTGTGACAGTGGCCGTAAACATCCCGTCTGTACTGTGACTGTGAGGCGGTAAAC	2010
Db	1861	CCTGCTTCCGAGTGTGACAGTGGCCGTAAACATCCCGTCTGTACTGTGAGGCGGTAAAC	1920
QY	2011	TGCGGCACTCAGGTGAAAGTCAACACAGCCATGAAATTCATCATCTGTGTGAACAGACA	2070
Db	1921	TGCGGCACTCAGGTGAAAGTCAACACAGCCATGAAATTCATCATCTGTGTGAACAGACA	1980
QY	2071	AGTTTCAAAAACTAA 2085	
Db	1981	AGTTTCAAAAACTAA 1995	
RESULT 4			
ABNS59646			
ID	ABNS59646	standard; cDNA; 3181 BP.	
XX	XX		
XX	AC	ABNS59646;	
XX	XX		
DT	28-JUN-2002	(first entry)	
DE	XX	Novel human coding sequence SEQ ID NO: 57.	
KM	XX	Human; antianemic; vulnereary; antiinflammatory; immunomodulator;	
KM	XX	antilethality; cerebroprotective; cyostatic; rheumatic; gene therapy;	
KM	XX	neuroprotective; antiparkinsonian; protein therapy; EST;	
KM	XX	expressed sequence tag; gene; ss.	
OS	XX	Homo sapiens.	
PN	XX	WO200222660-A2.	
PD	XX	21-MAR-2002.	
PF	XX	10-SEP-2001; 2001WO-US026015.	
PR	XX	11-SEP-2000; 2000US-00659671.	
PA	XX	(HYSE-) HYSEQ INC.	
PI	Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F,		

PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX MPI, 2002-282408/33.
DR P-PSDB; ABB97233.
XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Claim 1, SEQ ID NO 57; 509bp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention
XX
SQ Sequence 3181 BP; 756 A; 830 C; 879 G; 716 T; 0 U; 0 Other;
Query Match 60.4%; Score 1618; DB 6; Length 3181;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 709 GGGTCTGGGGGATGATGATCTCCCTTAAAGAAAGTGTCTCTGTGGCAAGTGA 768
DB 591 GGGTCTGGGGGATGATGATCTCCCTTAAAGAAAGTGTCTCTGTGGCAAGTGA 650
QY 769 GTTCTCAGCTTTGCTTCTCAGCTTCTCCAGACAAAGAAAGTGTCTCTGTGGAA 828
DB 651 GTTCTCAGCTTTGCTTCTCAGCTTCTCCAGACAAAGAAAGTGTCTCTGTGGAA 710
QY 829 CCCAGATCAGAGAGATTTGAGCCCGTGAAGAAATGAGAGAGATGGGAGCTT 888
DB 711 CCCAGATCAGAGAGATTTGAGCCCGTGAAGAAATGAGAGAGATGGGAGCTT 770
QY 889 GACCTGAACGGGAGCTTGTGTGTGCAACACCGGTGAAGATGCCAAACGCTCAAG 948
DB 771 GACCTGAACGGGAGCTTGTGTGTGCAACACCGGTGAAGATGCCAAACGCTCAAG 830
QY 949 GACCTGAACGGGAGCTTGTGTGTGCAACACCGGTGAAGATGCCAAACGCTCAAG 1008
DB 831 GACCTGAACGGGAGCTTGTGTGTGCAACACCGGTGAAGATGCCAAACGCTCAAG 890
QY 1009 TGCAGAGACCTGTGCAAGCTGTGTGAGCTTGTGAGCCCTGCAATGCAACGTTCTGCG 1068
DB 891 TGCAGAGACCTGTGCAAGCTGTGTGAGCTTGTGAGCCCTGCAATGCAACGTTCTGCG 950
QY 1069 GCTTGTGCTACTCGGAGCTGATGAGAGCGCTCTCTGTGTCTTACTGCGCTGCGCGT 1128
DB 951 GCTTGTGCTACTCGGAGCTGATGAGAGCGCTCTCTGTGTCTTACTGCGCTGCGCGT 1010
QY 1129 GAGCGGATCTGTAAAAACCAATCTCAACACCTCTGGAAGATATCTCATTCAGCAT 1188
DB 1011 GAGCGGATCTGTAAAAACCAATCTCAACACCTCTGGAAGATATCTCATTCAGCAT 1070
QY 1189 CCAGACAAAGATGGAGTGAAGAAATGCAAGATGATGATGATGATGATGATGATGATGAT 1248
DB 1071 CCAGACAAAGATGGAGTGAAGAAATGCAAGATGATGATGATGATGATGATGATGATGAT 1130
QY 1249 CAAGACATGCTGAGCCCAAGTCAAGCGGTCTTTTCTGATGAAGAAAGGAGTTCAAG 1308
DB 1131 CAAGACATGCTGAGCCCAAGTCAAGCGGTCTTTTCTGATGAAGAAAGGAGTTCAAG 1190
QY 1309 GACCTGCTGAGAGCTGTGAGAGCTTGAAGATGATGATGATGATGATGATGATGATGAT 1368
DB 1191 GACCTGCTGAGAGCTGTGAGAGCTTGAAGATGATGATGATGATGATGATGATGATGAT 1250
QY 1369 GTGTGCGGAGAGTGTCTGAGTACAGAAAGCAGCGCGCAGAGCTCCCACTGCCAGCA 1428

DB 1251 GTGTGCGGAGAGTGTCTGAGTACAGAAAGCAGCGCGCAGAGCTCCCACTGCCAGCA 1310
QY 1429 CCGAGAGGAGAGCAGAGAGCCCAAGCGCTCTGGGAGATGACATCTTCAGTCTGTCAGC 1488
DB 1311 CCGAGAGGAGAGCAGAGAGCCCAAGCGCTCTGGGAGATGACATCTTCAGTCTGTCAGC 1370
QY 1489 CTGACGACAGAGTCAAGATTAAGTGTGCTCTCTGCAAGAAAGCAGCGCTGTCAGC 1548
DB 1371 CTGACGACAGAGTCAAGATTAAGTGTGCTCTCTGCAAGAAAGCAGCGCTGTCAGC 1430
QY 1549 TGTGCTTCTCAGAGCCCAAGTCCAGACCGGAGAGCAGAGAGAGAGAGAGAGAGAGAGAG 1608
DB 1431 TGTGCTTCTCAGAGCCCAAGTCCAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1490
QY 1609 CTTCAAGATGTGCGGTGTGCTGCTGAGACCTTTCTGCACTGTAATCTGAGGCTGACCCG 1668
DB 1491 CTTCAAGATGTGCGGTGTGCTGCTGAGACCTTTCTGCACTGTAATCTGAGGCTGACCCG 1550
QY 1669 ACCGCTGCTAAGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728
DB 1551 ACCGCTGCTAAGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1610
QY 1729 GACGCGTCTGAAACAACAAGCTACAGATCAGATCCTGAAAGATTAATCTGAGAAC 1788
DB 1611 GACGCGTCTGAAACAACAAGCTACAGATCAGATCCTGAAAGATTAATCTGAGAAC 1670
QY 1789 AGAGTTTGAATGAGAAAAATGTTGACCGAGAGCTCTGTGCTTCCAGCGGAGAGT 1848
DB 1671 AGAGTTTGAATGAGAAAAATGTTGACCGAGAGCTCTGTGCTTCCAGCGGAGAGT 1730
QY 1849 TTTCTGCTGTGATTAAGAGTCAAGAGTCAAGAGAGACCGTCTGTGTAATCTGTGAGCTG 1908
DB 1731 TTTCTGCTGTGATTAAGAGTCAAGAGTCAAGAGAGACCGTCTGTGTAATCTGTGAGCTG 1790
QY 1909 CGAGCTTCCGTGAGCTGACCTATCAGTATCCGCAAGAACTTCTCTTCCAGTTGCCA 1968
DB 1791 CGAGCTTCCGTGAGCTGAGCTATCAGTATCAGAGAAACATTCCTCTCCAGTTGCCA 1850
QY 1969 GTGCGCTGAACATCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2028
DB 1851 GTGCGCTGAACATCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1910
QY 2029 GCTCAACAGCCATGAAATTCATATCTGTGAAACAGAAAGTTCAAAATCTAAGCA 2088
DB 1911 GCTCAACAGCCATGAAATTCATATCTGTGAAACAGAAAGTTCAAAATCTAAGCA 1970
QY 2089 TCCAGAGCCCTGAGAGCTTTCAGACCTGAGAGTGAAGAGAGCTGTTTAAATACA 2148
DB 1971 TCCAGAGCCCTGAGAGCTTTCAGACCTGAGAGTGAAGAGAGCTGTTTAAATACA 2030
QY 2149 GAGACAAGACGTCAGAGGTGTTTCAAGCCCCCTGAGAGAGAGAGAGAGAGAGAGAG 2208
DB 2031 GAGACAAGACGTCAGAGGTGTTTCAAGCCCCCTGAGAGAGAGAGAGAGAGAGAGAG 2090
QY 2209 CAGGTGCTGTGGGTGATCTTCTGTGAGAGCTTTTAACTCTGATGAGAGAGAGAGAGAG 2268
DB 2091 CAGGTGCTGTGGGTGATCTTCTGTGAGAGCTTTTAACTCTGATGAGAGAGAGAGAG 2148
QY 2269 GAGCCCCGAG 2328
DB 2149 GAGCCCCGAG 2208
QY 2329 CAGCAGCAG 2388
DB 2209 CAGCAGCAG 2268
QY 2389 GCTCTTTTGTACATTTTCCGAAATCAAGTAAAGAGAGAGAGAGAGAGAGAGAGAG 2448
DB 2269 GCTCTTTTGTACATTTTCCGAAATCAAGTAAAGAGAGAGAGAGAGAGAGAGAGAG 2328
QY 2449 TCAAGGAG 2508

Db 2329 TCAGGAGAGAGGCAAGTTTATCAAAAAACATTGTTTCAGAGAGAGGACATAAGTTTA 2388
 QY 2509 CAGCCTACAGAGAGTACACAAATATCTGCTGCTGAGAAAAACAAGCATTATTAATTT 2568
 CC CAGCCTACAGAGAGTACACAAATATCTGCTGCTGAGAAAAACAAGCATTATTAATTT 2448
 Db 2389 CAGCCTACAGAGAGTACACAAATATCTGCTGCTGAGAAAAACAAGCATTATTAATTT 2448
 QY 2569 TTTATTTTAAATAGTTTGGTGGCTTATCTTCTAATAGATTTAATGTCAAACTGTAC 2628
 Db 2449 TTTATTTTAAATAGTTTGGTGGCTTATCTTCTAATAGATTTAATGTCAAACTGTAC 2508
 QY 2629 ACAATATATATATATTTATTAATTTACAAATTGAC 2661
 Db 2509 ACAATATATATATATTTATTAATTTACAAATTGAC 2541

RESULT 5
 AAH14556
 ID AAH14556 standard; cDNA; 3138 BP.
 AC AAH14556;
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:12127.
 XX
 KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000BP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036- 99JP-00300253.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JUN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 PS Claim 8; SEQ ID NO 12127; 2537bp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AA82446 to AA85893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 3138 BP; 738 A; 824 C; 873 G; 703 T; 0 U; 0 Other;
 Query Match 54.7%; Score 1465; DB 4; Length 3138;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1945; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 QY 709 GGGTCGGGGGGGNGGAGATCCCGCTAAAGGAAGTGGCCCTGCTGGCAAGTATGA 768
 Db 560 GGGCTCGGGGGGAGGAGATCTCCCTTAAGGAAGTGGCTCTGTGGCAAGTATGA 619
 QY 769 GTCTCAGCTTTCCTCAGCTCTCCAGACAGAAAGATGCTCTCTTTCGTCTGGAA 828
 Db 620 GTCTCAGCTTTCCTCAGCTCTCCAGACAGAAAGATGCTCTCTTTCGTCTGGAA 679
 QY 829 CCCGAGATCAGAGAGATTTGGAGCCCGTGAAGAAAGAAATGAGAGAGATGGGACCTT 888
 Db 680 CCCGAGATCAGAGAGATTTGGAGCCCGAAGAAAGAAATGAGAGATGGGACCTT 739
 QY 889 GACCTGAAGGGGCAATGTTGGTGGCACAACCGGCTAGAAATGCCAAACGCTCCAGAG 948
 Db 740 GACCTGAAGGGGCAATGTTGGTGGCACAACCGGCTAGAAATGCCAAACGCTCCAGAG 799
 QY 949 GACCTCAGAGCAGCGGCTGGGAGAGCCAGACAAAGATGAGAGAGACGCTGACATGATCATC 1008
 Db 800 GACCTCAGAGCAGCGGCTGGGAGAGCCAGACAAAGATGAGAGAGACGCTGACATGATCATC 859
 QY 1009 TGGCAGAACCTGCTGCACAGATGCTGCTGAGTTTGCAGCCCTGATGACACAGTTTGGCGG 1068
 Db 860 TGGCAGAACCTGCTGCACAGATGCTGCTGAGTTTGCAGCCCTGATGACACAGTTTGGCGG 919
 QY 1069 GCTTGCTACTCGGGGCTGGATGGAGGCGTGCCTGCTGCTCAACCTGCGCGCTGCCGCG 1128
 Db 920 GCTTGCTACTCGGGGCTGGATGGAGGCGTGCCTGCTGCTCAACCTGCGCGCTGCCGCG 979
 QY 1129 GAGCGGATCTGTAAAAACAACATCTCTCAACAACCTCTGTGAGAGCATATCTTCAGCAT 1188
 Db 980 GAGCGGATCTGTAAAAACAACATCTCTCAACAACCTCTGTGAGAGCATATCTTCAGCAT 1039
 QY 1189 CCAGACAAAGATCGGAGTGAAGAGATGTGCAGAGATGATGCCAGATTAATCACT 1248
 Db 1040 CCAGACAAAGATCGGAGTGAAGAGATGTGCAGAGATGATGCCAGATTAATCACT 1099
 QY 1249 CAAGACATGCTGAGCCCAAGAGTCAAGGCGCTTTTCTGATGAAGAGGAGTTCAGAG 1308
 Db 1100 CAAGACATGCTGAGCCCAAGAGTCAAGGCGCTTTTCTGATGAAGAGGAGTTCAGAG 1159
 QY 1309 GACCTGCTGAGCTGTCAAGAGTGAAGTGAAGTCTCTGACACATTAGCCAGCATATGCTC 1368
 Db 1160 GACCTGCTGAGCTGTCAAGAGTGAAGTGAAGTCTCTGACACATTAGCCAGCATATGCTC 1219
 QY 1369 GTGTGCGGCGAGTGTCTGATGATGAAGAGGAGGCGGAGCTTCCCACTGCCACGA 1428
 Db 1220 GTGTGCGGCGAGTGTCTGATGATGAAGAGGAGGCGGAGCTTCCCACTGCCACGA 1279
 QY 1429 CCCGAGGGCGAGCCAGAGACCCCAAGGCGCTGGGGAGATGACCTCTCAGAGTCCGTGACG 1488
 Db 1280 CCCGAGGGCGAGCCAGAGACCCCAAGGCGCTGGGGAGATGACCTCTCAGAGTCCGTGACG 1339
 QY 1489 CTGAGCAGCAGATCTCAGATTAAGTGTGCTCTGCAAGAGAACCCCTGTGACAC 1548
 Db 1340 CTGAGCAGCAGATCTCAGATTAAGTGTGCTCTGCAAGAGAACCCCTGTGACAC 1399
 QY 1549 TGTCTCTTCAGCCCATATCCCGAGAGCGAGAGCGGAGCAGAGACCCGCTGTGCGC 1608
 Db 1400 TGTCTCTTCAGCCCATATCCCGAGAGCGGAGAGCGGAGCAGAGACCCGCTGTGCGC 1459
 QY 1609 CCTGAGAGTGTGGGCTGTGCTGAGCTTCTTCTGACCTGTATGTGGGGCTGACCCGG 1668

Db 1460 CCTCAGCAGTGTGCGGTCTGCTGACGCTTTCTGCACTGTAAGTGGGCTGACCCCG 1519
 QY 1669 ACCGGCTGCTACGGCTGCTGCGCCCGTTTGTGAGCTCAACCTGGGTGCAAGTGTCTG 1728
 Db 1520 ACCGGCTGCTACGGCTGCTGCGCCCGTTTGTGAGCTCAACCTGGGTGCAAGTGTCTG 1579
 QY 1729 GACGGGTGCTGACCAACAACAGCTACAGAGTCAAGTCTGGAAGATTACTTGGCAACC 1788
 Db 1580 GACGGGTGCTGACCAACAACAGCTACAGAGTCAAGTCTGGAAGATTACTTGGCAACC 1539
 QY 1789 AGAGGTTTGAATGAGAAAAATGTTGACCGAGAGCTCTGTGCTCTCCAGCGGGAGTG 1848
 Db 1640 AGAGGTTTGAATGAGAAAAATGTTGACCGAGAGCTCTGTGCTCTCCAGCGGGAGTG 1699
 QY 1849 TTTCTGCTGTCTGATTAACAGAGTCAAGGAGACACCTTGTGTGTTACTGTGTGCTG 1908
 Db 1700 TTTCTGCTGTCTGATTAACAGAGTCAAGGAGACACCTTGTGTGTTACTGTGTGCTG 1759
 QY 1909 CCGAGCTTCCGTAGCTGACCTATCAGTATCGGCAAGAACATTCCTGCTTCCGAGTTGCCA 1968
 Db 1760 CCGAGCTTCCGTAGCTGACCTATCAGTATCAGCAAGAACATTCCTGCTTCCGAGTTGCCA 1819
 QY 1969 GTGGCGGTAAATCCGCTCTGACTGTAAGTGGGCGGTAACTGCGCACTCAGGTGAAA 2028
 Db 1820 GTGGCGGTAAATCCGCTCTGACTGTAAGTGGGCGGTAACTGCGCACTCAGGTGAAA 1879
 QY 2029 GCTCAGCAGCGCCATGAAATTCATATCTGTGAAACAGACAGGTTCAAAAATAAGCA 2088
 Db 1880 GCTCAGCAGCGCCATGAAATTCATATCTGTGAAACAGACAGGTTCAAAAATAAGCA 1939
 QY 2089 TCCAGAGCCCTGAGCAGCTTTGAGCACTGAGGTGAGAGAGCGTGTGTTTAAATATCA 2148
 Db 1940 TCCAGAGCCCTGAGCAGCTTTGAGCACTGAGGTGAGAGAGCGTGTGTTTAAATATCA 1999
 QY 2149 GAGACAGACGCTCAAGGTGTTTCAAGCCCTGAGGAGAGAGACGAGGCTCTCCGA 2208
 Db 2000 GAGGACAGACGCTCAAGGTGTTTCAAGCCCTGAGGAGAGAGACGAGGCTCTCCGA 2059
 QY 2209 CAGGTGCTCTGGGTGATCTTTCTGTGAGAGCTTTTAACTTGAAGTGAAGACCTTCCCA 2268
 Db 2060 CAGGTGCTCTGGGTGATCTTTCTGTGAGAGCTTTTAACTTGAAGTGAAGACCTTCCCA 2117
 QY 2269 GAGCCCGGGGGGCGGAGCCGCTCTGTGAGAGGCTGGGAGGAGGCTGTGTGAGCAT 2328
 Db 2118 GAGCCCGGGGGGCGGAGCCGCTCTGTGAGAGGCTGGGAGGAGGCTGTGTGAGCAT 2177
 QY 2329 CAGCAGCAGAGAGAGAGCTTTCTGTAACTGCGCGCTGCCCGAGAGGCGCAGTTT 2388
 Db 2178 CAGCAGCAGAGAGAGAGCTTTCTGTAACTGCGCGCTGCCCGAGAGGCGCAGTTT 2237
 QY 2389 GCTCTTTTGTACATTTTCCGAACTACAGTTAAAGCAAGAGTCTGTTTTCAGGAAAAATT 2448
 Db 2238 GCTCTTTTGTACATTTTCCGAACTACAGTTAAAGCAAGAGTCTGTTTTCAGGAAAAATT 2297
 QY 2449 TCAGGAGAGAGAGAGAGTTTATCAAAAACATGTTTCAGGAGAGGAGCATTAAGTTTA 2508
 Db 2298 TCAGGAGAGAGAGAGAGTTTATCAAAAACATGTTTCAGGAGAGGAGCATTAAGTTTA 2357
 QY 2509 CAGCCTACAGAGAGTACACAAATCTGCTGCTGAGGAAAAACAACAGATTTTATCTAATT 2568
 Db 2358 CAGCCTACAGAGAGTACACAAATCTGCTGCTGAGGAAAAACAACAGATTTTATCTAATT 2417
 QY 2569 TTTATTTTAAATAGTTTGTGCTTATCTTAAATGAATTTAAATGTCACAACTGTAGC 2628
 Db 2418 TTTATTTTAAATAGTTTGTGCTTATCTTAAATGAATTTAAATGTCACAACTGTAGC 2477
 QY 2629 ACAATATATATATATATATATATATCAAAATTGAC 2661
 Db 2478 ACAATATATATATATATATATATATCAAAATTGAC 2510

RESULT 6
 AAI88903/c

ID AAI88903 standard; cDNA; 2259 BP.
 AC AAI88903; c
 DT 06-NOV-2001 (first entry)
 XX Human polynucleotide SEQ ID NO 8963.
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 EN WO200164835-A2.
 XX 07-SEP-2001.
 PD 26-FEB-2001; 2001MO-US004927.
 PF 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Dmanac RT;
 XX WPI; 2001-514838/56.
 DR P-PSDB; AAO08972.
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukaemia, inflammation and immune disorders.
 XX Claim 1; SEQ ID NO 8963; 1399bp + Sequence Listing; English.
 PS The invention relates to human polynucleotides (AAI9941-AAI99841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2259 BP; 531 A; 612 C; 615 G; 501 T; 0 U; 0 Other;
 Query Match 38.2%; Score 1024; DB 4; Length 2259;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1304; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
 QY 1354 AGCCAGCCATAGCTGCTGTGCGGAGTGTCTGAGTACAGAGGCGGCGAGCCT 1413
 Db 1965 AGCCAGCCATAGCTGCTGTGCGGAGTGTCTGAGTACAGAGGCGGCGAGCCT 1906
 QY 1414 CCCAGTGGCCAGAGACCCGAGGGCGGAGGAGGCCCAAGGCCCTGGGGAGATGACCC 1473
 Db 1905 CCCAGTGGCCAGAGACCCGAGGGCGGAGGAGGCCCAAGGCCCTGGGGAGATGACCC 1846
 QY 1474 TCCAGCTCCGTAGCTGACAGACAGAGTCAAGATTACGTGTGCTCTGCAAGAGAC 1533
 Db 1845 TCCAGCTCCGTAGCTGACAGACAGAGTCAAGATTACGTGTGCTCTGCAAGAGAC 1786
 QY 1534 CAGCCCTGTGCACTGCTGCTTCCAGGCCATGCCCCGAGAGCGGAGCGGAGAG 1593
 Db 1785 CAGCCCTGTGCACTGCTGCTTCCAGGCCATGCCCCGAGAGCGGAGCGGAGAG 1726
 QY 1594 GACCCGCGTGTGCGCCCTCAGAGAGTGTGGGTCTGCTGACGCTTCTGCACTGTAC 1653

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Db      1725 GACCCCGCTGTCCGCTTACGACGCTGCGCTGCTGACCTTCTGCGACCTGTGAC 1666
Qy      1654 TGGGGGTGCAACCCGGAACCGGCTGCTACGCGTGCCTGCGCCGCTTTTGTGAGCTCAACTG 1713
Db      1665 TGGGGGTGCAACCCGGAACCGGCTGCTACGCGTGCCTGCGCCGCTTTTGTGAGCTCAACTG 1606
Qy      1714 GGTGACAAAGTGTGTGGAACCGGCTGCTGAACAACAAGCTACGAGTCAAGACATCTGAAG 1773
Db      1605 GGTGACAAAGTGTGTGGAACCGGCTGCTGAACAACAAGCTACGAGTCAAGACATCTGAAG 1546
Qy      1774 AATTACCTGGCAACAGAGGTTTGAATGAGGAAAAAATGATGTCGAGAGCCGCGGCT 1833
Db      1545 AATTACCTGGCAACAGAGGTTTGAATGAGGAAAAAATGATGTCGAGAGCCGCGGCT 1486
Qy      1834 CTCACGCGGGAGTGTCTGTCTGTCTGTATTCAGAGTACGAGGACACCGTTCTGTGT 1893
Db      1485 CTCACGCGGGAGTGTCTGTCTGTCTGTATTCAGAGTACGAGGACACCGTTCTGTGT 1426
Qy      1894 TACTGTGTGGCTGTGGGAGCTTCCGTGAGCTGACCTATCAGTATCGGACAACTTCT 1953
Db      1425 TACTGTGTGGCTGTGGGAGCTTCCGTGAGCTGACCTATCAGTATCGGACAACTTCT 1366
Qy      1954 GCTTCGAGTGTGCAAGTGCCTGAAATCATCCGCTCTGACTGCTACTGGGCGGTAACTGC 2013
Db      1365 GCTTCGAGTGTGCAAGTGCCTGAAATCATCCGCTCTGACTGCTACTGGGCGGTAACTGC 1306
Qy      2014 CGCACTCAGGTGAAGCTCAACACGCGCATGAAATTCATCATATCTGTGAACAGACAG 2073
Db      1305 CGCACTCAGGTGAAGCTCAACACGCGCATGAAATTCATCATATCTGTGAACAGACAG 1246
Qy      2074 TTCAAAAAATAGATCCAGAGGCGCTGAGAGCTTTCAGCACTGAGAGTGAAGAGAGG 2133
Db      1245 TTCAAAAAATAGATCCAGAGGCGCTGAGAGCTTTCAGCACTGAGAGTGAAGAGAGG 1186
Qy      2134 TCTTTTAAATAACAGAGACAAAGCAAGTCAAGTGTTCACAGCCCTGAGGAGAGG 2193
Db      1185 TCTTTTAAATAACAGAGACAAAGCAAGTCAAGTGTTCACAGCCCTGAGGAGAGG 1126
Qy      2194 AGCGAGGCTCTCCGACAGTGTCTCTGGGGTACTCTTCTGTGAGAGCTTTTAACTCTGA 2253
Db      1125 AGCGAGGCTCTCCGACAGTGTCTCTGGGGTACTCTTCTGTGAGAGCTTTTAACTCTGA 1068
Qy      2254 GTGAGACCTCCCGACAGAGCCCGGGGGGCGGAGCCCGCTCTGTGAGAGCTGGGAG 2313
Db      1067 GTGAGACCTCCCGACAGAGCCCGGGGGGCGGAGCCCGCTCTGTGAGAGCTGGGAG 1008
Qy      2314 GGTCTGTGTGATCAGCAGACAGACGAAAGCTTTCTGTAAATGCGGCGCTCCGCG 2373
Db      1007 GGTCTGTGTGATCAGCAGACAGACGAAAGCTTTCTGTAAATGCGGCGCTCCGCG 948
Qy      2374 GAGAGGGGAGTGTGTCTTTTGTACATTTTCCGAAACTACAGTTTAAAGCAAGTCTG 2433
Db      947 GAGAGGGGAGTGTGTCTTTTGTACATTTTCCGAAACTACAGTTTAAAGCAAGTCTG 888
Qy      2434 TTTTCAAGAAAAGTTTCAAGGAGAGGCAAGTTTATCAAAAACATTTTCAAGAGAA 2493
Db      887 TTTTCAAGAAAAGTTTCAAGGAGAGGCAAGTTTATCAAAAACATTTTCAAGAGAA 828
Qy      2494 GGGAGCATTAAGTTTACAGCTTACAGACGTACACAAATTCCTGCTGTGGGAAAAACA 2553
Db      827 GGGAGCATTAAGTTTACAGCTTACAGACGTACACAAATTCCTGCTGTGGGAAAAACA 768
Qy      2554 GCATTTTATCTATTTTATTTTATTTATTTAGTTTGTGCTTATCTTCTAATTAAGTTTAA 2613
Db      767 GCATTTTATCTATTTTATTTTATTTATTTAGTTTGTGCTTATCTTCTAATTAAGTTTAA 708
Qy      2614 GTCAAACTGTAGCAAAATATATATTTATTTATTTATTTAATTTGAC 2661
Db      707 GTCAAACTGTAGCAAAATATATATTTATTTATTTAATTTGAC 660

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RESULT 7

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ADMO3388
ID      ADMO3388 standard; cDNA; 2448 BP.
XX
XX
AC      ADMO3388;
XX
XX      20-MAY-2004 (first entry)
XX
XX      Human cDNA of the invention SEQ ID NO:2073.
DE
XX      ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX      Homo sapiens.
OS
XX      EP1347046-A1.
PN
XX      24-SEP-2003.
PD
XX      12-APR-2002; 2002EP-00008400.
PF
XX      22-MAR-2002; 2002JP-00137785.
PR
XX      (REAS-) RES ASSOC BIOTECHNOLOGY.
PA
XX      Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI      Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI      Seki N, Yoshikawa T, Otsuka M, Negahari K, Masuno Y;
XX      WPI; 2003-723558/69.
DR      P-Psdb; ADM05831.
XX
XX      New polynucleotides and polypeptides are useful in gene therapy, for
PT      developing a diagnostic marker or medicines for regulating their
PT      expression and activity, or as a target of gene therapy.
XX
XX      Claim 1; SEQ ID NO 2073; 305bp; English.
PS
XX
XX      The invention relates to a novel human polynucleotide and the encoded
CC      polypeptide. A polynucleotide of the invention may have a use in gene
CC      therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC      as a primer for synthesizing the polynucleotide or as a probe for
CC      detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC      useful in gene therapy, for developing a diagnostic marker or medicines
CC      for regulating their expression and activity, or as a target of gene
CC      therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC      are useful as pharmaceutical agents. The present sequence represents a
CC      cDNA sequence of the invention.
XX
XX      Sequence 2448 BP; 618 A; 624 C; 661 G; 545 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      35.2%; Score 944; DB 11; Length 2448;
XX      Best Local Similarity 99.9%; Pred. No. 0;
XX      Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      708 TGGGCTGCGGGGTGTGATCTCCCTTAAAGAAAGTGTCCCTGTGGAAGTATGA 767
Db      357 TGGGCTGCGGGGTGTGATCTCCCTTAAAGAAAGTGTCCCTGTGGAAGTATGA 416
Qy      768 AGTCTCAGCTTGTCTTCACTCTCCAGACAGAAAGCTGCTCTTTTGTGCTTGA 827
Db      417 AGTCTCAGCTTGTCTTCACTCTCCAGACAGAAAGCTGCTCTTTTGTGCTTGA 476
Qy      828 ACCCGAGATGAGAGATTTTGGAGCCCGTGAAGAAATGAGAGAGATGGGGACCT 887
Db      477 ACCCGAGATGAGAGATTTTGGAGCCCGTGAAGAAATGAGAGAGATGGGGACCT 536
Qy      888 TGACCTGAACGGGAGTGTGTGTGCAACAACCGCTGAGAAATCCCAACCGTCCAGA 947
Db      537 TGACCTGAACGGGAGTGTGTGTGCAACAACCGCTGAGAAATCCCAACCGTCCAGA 596
Qy      948 GGAAGTCAAGACAGCGGCTGGGAAGCCAGACAGATGAGAGAGCGTGAACATGATCAT 1007
Db      597 GGAAGTCAAGACAGCGGCTGGGAAGCCAGACAGATGAGAGAGCGTGAACATGATCAT 656

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PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 12-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246478P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM,
XX
DR WPI; 2001-488783/53.

DR P-PSDB; AAU15856.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 1; SEQ ID NO 22; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
Query Match 28.6%; Score 765; DB 4; Length 1311;
Best Local Similarity 100.0%; Pred. No. 2,8e-273;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 710 GGTCTGGGGGGTGGTGGCATCTCCCTTAAGAAAGTGTCTCTGTGGCAAGTATGAG 769
Db GGTCTGGGGGGTGGTGGCATCTCCCTTAAGAAAGTGTCTCTGTGGCAAGTATGAG 442
QY 770 TCTCCAGCTTGGCTCAGCTCTCCCAAGCAGAAAGTGTCTCTGTGGCAAGTATGAG 829
Db TCTCCAGCTTGGCTCAGCTCTCCCAAGCAGAAAGTGTCTCTGTGGCAAGTATGAG 502
QY 443 TCTCCAGCTTGGCTCAGCTCTCCCAAGCAGAAAGTGTCTCTGTGGCAAGTATGAG 502
Db TCTCCAGCTTGGCTCAGCTCTCCCAAGCAGAAAGTGTCTCTGTGGCAAGTATGAG 889
QY 830 CCCAGGATCAGAGAGATTTGAGCCCGTGAAGAAAGTATGAGAGATGGAGACCTTG 889
Db CCCAGGATCAGAGAGATTTGAGCCCGTGAAGAAAGTATGAGAGATGGAGACCTTG 562
QY 503 CCCAGGATCAGAGAGATTTGAGCCCGTGAAGAAAGTATGAGAGATGGAGACCTTG 562
Db CCCAGGATCAGAGAGATTTGAGCCCGTGAAGAAAGTATGAGAGATGGAGACCTTG 949
QY 890 AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 949
Db AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 622
QY 563 AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 622
Db AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 1069
QY 950 AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 1069
Db AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 682
QY 623 AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 682
Db AACTGAACGGGCACTTTGGTGGTCCCAACCGCGTAAAGAAAGTATGAGAGATGGAG 742
QY 1010 GCCAGAACCTGCTGACGACCTGCTGAGTTTGACGCCCTGATGACACGTTTGGCGGG 1069
Db GCCAGAACCTGCTGACGACCTGCTGAGTTTGACGCCCTGATGACACGTTTGGCGGG 742
QY 683 GCCAGAACCTGCTGACGACCTGCTGAGTTTGACGCCCTGATGACACGTTTGGCGGG 742
Db GCCAGAACCTGCTGACGACCTGCTGAGTTTGACGCCCTGATGACACGTTTGGCGGG 1129
QY 1070 CTTGCTACTCGGGGCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129
Db CTTGCTACTCGGGGCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 802
QY 743 CTTGCTACTCGGGGCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 802
Db CTTGCTACTCGGGGCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
QY 1130 AGCGGATCTGTAAACCAATCTCTCAACCACTCTGTGAGAGATCACTATCCAGATC 1189
Db AGCGGATCTGTAAACCAATCTCTCAACCACTCTGTGAGAGATCACTATCCAGATC 862
QY 803 AGCGGATCTGTAAACCAATCTCTCAACCACTCTGTGAGAGATCACTATCCAGATC 862
Db AGCGGATCTGTAAACCAATCTCTCAACCACTCTGTGAGAGATCACTATCCAGATC 1249
QY 1190 CAGCAAGAGTCCGAGTGAAGAGATGTGCAAGTATGAGTCCAGGAATTAATCACTC 1249
Db CAGCAAGAGTCCGAGTGAAGAGATGTGCAAGTATGAGTCCAGGAATTAATCACTC 922

QY 1250 AAGACATGCTGACAGCCCAAGTCAAGCGGCTTTTCTGATGAGAGGAGTTCAAGG 1309
 |||||
 DB 923 AAGACATGCTGACAGCCCAAGTCAAGCGGCTTTTCTGATGAGAGGAGTTCAAGG 982
 |||||
 QY 1310 ACCTGCTGAGCTGTCAAGCTTGAAGTCTTCAAGCATTAAGCCCAATACGTCG 1369
 |||||
 DB 983 ACCTGCTGAGCTGTCAAGCTTGAAGTCTTCAAGCATTAAGCCCAATACGTCG 1042
 |||||
 QY 1370 TGTGCGGCGAGCTGTCTGATGAGAGGAGGCGGCGGCGGCTCTCCCACTGCCAGAC 1429
 |||||
 DB 1043 TGTGCGGCGAGCTGTCTGATGAGAGGAGGCGGCGGCGGCTCTCCCACTGCCAGAC 1102
 |||||
 QY 1430 CCGAGGCGGAGCCAGAGCCCAAGGCGGCTGAGGAGTGAACCT 1474
 |||||
 DB 1103 CCGAGGCGGAGCCAGAGCCCAAGGCGGCTGAGGAGTGAACCT 1147
 |||||
 RESULT 9
 ABX73184
 ID ABX73184 standard; DNA; 1311 BP.
 XX
 AC ABX73184;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Human novel polynucleotide #12.
 XX
 KW Human; gene; de; neural disorder; immune system disorder; renal disorder;
 KW muscular disorder; respiratory disease; reproductive disorder;
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
 KW cardiovascular; nephrotropic; cytosolic; antiallergic; thrombolytic;
 KW haemostatic; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN US2002132753-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 17-JAN-2001; 2001US-00764864.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218230P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226688P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234979P.

PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251566P.
 PR 08-DEC-2000; 2000US-0251688P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR
 XX
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 DR WPI; 2003-147444/14.
 DR P-PSDB; ABUS4924.
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular, or
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.
 XX
 XX
 PS Claim 1; SEQ ID NO 22; 402pp; English.
 XX
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
 CC human novel polynucleotides of the invention
 XX
 SO Sequence 1311 BP; 306 A; 359 C; 399 G; 239 T; 0 U; 8 Other;
 Query Match 28.6%; Score 765; DB 8; Length 1311;
 Best Local Similarity 100.0%; Pred. No. 2.8e-273; Indels 0; Gaps 0;
 Matches 765; Conservative 0; Mismatches 0;
 QY 710 GGTCTGGGGGTGGTGCATCTCCCTAAAGAAAGTGTGCTCTGTGGCAAGATGAAG 769
 |||||
 DB 383 GGTCTGGGGGTGGTGCATCTCCCTAAAGAAAGTGTGCTCTGTGGCAAGATGAAG 442
 |||||
 QY 770 TCTCAGCTTTGCTCAGCTCTCCAGACAGAAAGACTCGTCTTTTGTGCTGGAAC 829
 |||||
 DB 443 TCTCAGCTTTGCTCAGCTCTCCAGACAGAAAGACTCGTCTTTTGTGCTGGAAC 502
 |||||
 QY 830 CCGAGATCAGAGAGATTTTGAAGCCCGTGAAGAAAGAAATGAGAGAGATGGGACCTTG 889
 |||||
 DB 503 CCGAGATCAGAGAGATTTTGAAGCCCGTGAAGAAAGAAATGAGAGAGATGGGACCTTG 562
 |||||
 QY 890 ACCTGAACGGGAGTGTGTGTGCAACACCGGTGAATGCCCAACCGTCCAGAGG 949
 |||||

Db 563 ACCTGAACGGGCACTTGTGTCGACACACCGGCTAGAAATGCCCCAACCCCTCCACGAGG 622
 QY 950 ACCTCAGAGCAGCGCTGGAGACCCAGACAAGATGAGAGACGCTGACATGATCATCT 1009
 Db 623 ACCTCAGAGCAGCGCTGGAGACCCAGACAAGATGAGAGACGCTGACATGATCATCT 682
 QY 1010 GCCAGACCTGCTGACAGCATGCTGATGAGTTTGACAGCCCTGTCATGACACGTTTGGCGG 1069
 Db 683 GCCAGAGCCTGCTGACAGCATGCTGATGAGTTTGACAGCCCTGTCATGACACGTTTGGCGG 742
 QY 1070 CTGTCTACTCGGGCTGATGAGAGCGCTGCTCCTGATGCTTACCTGACCGCTGCTCCGCTG 1129
 Db 743 CTGTCTACTCGGGCTGATGAGAGCGCTGCTCCTGATGCTTACCTGACCGCTGCTCCGCTG 802
 QY 1130 AGCGATCTGTAAACCAATCTCTCAACACCTCGTGAAAGCATCTTCATCCAGCATC 1189
 Db 803 AGCGATCTGTAAACCAATCTCTCAACACCTCGTGAAAGCATCTTCATCCAGCATC 862
 QY 1190 CAGACAAAGTGCAGTGAAGAAAGATGTCAGAAAGTATGATGTCAGAGAAATTAATCATCTC 1249
 Db 863 CAGACAAAGTGCAGTGAAGAAAGATGTCAGAAAGTATGATGTCAGAGAAATTAATCATCTC 922
 QY 1250 AAGACATGCTGACAGCCCAAGTCAAGCGGCTCTTTTCTGATGAAGAGGAGTTTCAGAG 1309
 Db 923 AAGACATGCTGACAGCCCAAGTCAAGCGGCTCTTTTCTGATGAAGAGGAGTTTCAGAG 982
 QY 1310 ACTTGTGAGAGCTGTCAAGAGTTGAAGATGCTCTCAACATTAGCCAGCCATACGTCG 1369
 Db 983 ACTTGTGAGAGCTGTCAAGAGTTGAAGATGCTCTCAACATTAGCCAGCCATACGTCG 1042
 QY 1370 TGTGCGGAGAGTGTCTGAGATGACAAAGGAGGCGGAGCTCCCACTGCGCCAGCAGC 1429
 Db 1043 TGTGCGGAGAGTGTCTGAGATGACAAAGGAGGCGGAGCTCCCACTGCGCCAGCAGC 1102
 QY 1430 CCGAGGCGCAGAGCCAGGACCCCAAGGAGGAGGAGTCAACCTT 1474
 Db 1103 CCGAGGCGCAGAGCCAGGACCCCAAGGAGGAGGAGTCAACCTT 1147
 RESULT 10
 ADA52592
 ID ADA52592 standard; cDNA; 2186 BP.
 AC
 XX
 ADAS2592;
 AC
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human coding sequence, SEQ ID 160.
 XX
 DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KM Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KM Inflammatory disease; osteoporosis; neurological disease; gene; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR P-PSDB; ADA54231.

XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 1; SEQ ID NO 160; 205bp; English.
 CC
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 2186 BP; 493 A; 555 C; 539 G; 599 T; 0 U; 0 Other;
 Query Match 23.6%; Score 633; DB 10; Length 2186;
 Best Local Similarity 99.7%; Pred. No. 1.8e-224;
 Matches 863; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
 QY 1796 TGACATGGAAGAAACATGTTGACCGAGAGCTGTGAGCTTCTCAAGCGGAGTGTTCGC 1855
 Db 695 TGACATGGAAGAAACATGTTGACCGAGAGCTGTGAGCTTCTCAAGCGGAGTGTTCGC 754
 QY 1886 TGTCTGATTACAGAGTCAAGGAGACACCGTCTGTGTTACTGCTGTGCGCTGCGACCT 1915
 Db 755 TGTCTGATTACAGAGTCAAGGAGACACCGTCTGTGTTACTGCTGTGCGCTGCGACCT 814
 QY 1916 TCCGTGAGCTGACCTATCATGATGCGGAGAAACATTCCTGCTCGAGATGCGACGTCG 1975
 Db 815 TCCGTGAGCTGACCTATCATGATGCGGAGAAACATTCCTGCTCGAGATGCGACGTCG 874
 QY 1976 TAACTCCCGTCTGACTGCTACTGCGGCGGTAACTGCGCACTCAGGTGAAGTCAAC 2035
 Db 875 TAACTCCCGTCTGACTGCTACTGCGGCGGTAACTGCGCACTCAGGTGAAGTCAAC 934
 QY 2036 ACGCATGAATTCATCATATCTGTGAAACAGACAAAGTTCAAAAACCTAACATCCAGAG 2095
 Db 935 ACGCATGAATTCATCATATCTGTGAAACAGACAAAGTTCAAAAACCTAACATCCAGAG 994
 QY 2096 GCCCTGAGCAGCTTTCAGACCTGAGAGTGAAGAGCGTGTTTTAAATACAGAGCAA 2155
 Db 995 GCCCTGAGCAGCTTTCAGACCTGAGAGTGAAGAGCGTGTTTTAAATACAGAGCAA 1054
 QY 2156 GCAAGTCAAGGTGTTTTCACAGCCCTGAGAGGAAAGGACGACAGGTCTCCGACAGGTGC 2215
 Db 1055 ACAAGTCAAGGTGTTTTCACAGCCCTGAGAGGAAAGGACGACAGGTCTCCGACAGGTGC 1114
 QY 2216 TCTGAGGTGACTCTTCTGTGAGAGCTTTTAACTCTGAGTGAACCTCCCAAGAGCCCC 2275
 Db 1115 TCTGAGGTGACTCTTCTGTGAGAG--TTTAACTCTGAGTGAACCTCCCAAGAGCCCC 1172
 QY 2276 GGGGCGCGCAGCCCGCCCTCTGAGAGCGTGGGACAGGCTGCTGTGATCAGCAGC 2335
 Db 1173 GGGGCGCGCAGCCCGCCCTCTGAGAGCGTGGGACAGGCTGCTGTGATCAGCAGC 1232
 QY 2336 AGAGCAGAGCTTCTGTGACATGCGGCGTCCCGCGAGAGGGGAGTTTCTCTT 2395
 Db 1233 AGAGCAGAGCTTCTGTGACATGCGGCGTCCCGCGAGAGGGGAGTTTCTCTT 1292
 QY 2396 TGTACATTTTCCGAACCTACAGTTAAGCAGAACTGTGTTTTCAGAAAAGTTTCAAGG 2455
 Db 1293 TGTACATTTTCCGAACCTACAGTTAAGCAGAACTGTGTTTTCAGAAAAGTTTCAAGG 1352
 QY 2456 AGAAGGCGCAAGTTATCAAAAACATTTGTTTCAAGAGAAAGGACATTAAGCTTACGCTTA 2515
 Db 1353 AGAAGGCGCAAGTTATCAAAAACATTTGTTTCAAGAGAAAGGACATTAAGCTTACGCTTA 1412
 QY 2516 CAGAGCGTACCAATATCTGCTGCTGAGGAAACCAAGCATTTTATCTATTTTATTT 2575
 Db 1413 CAGAGCGTACCAATATCTGCTGCTGAGGAAACCAAGCATTTTATCTATTTTATTT 1472
 QY 2576 TAAATAGTTGTGCTTATCTTCTAATAGATTAAATGTCACAACTGACCAATA 2635

DB 1473 TAATAGTTTGCTTATCTTAATAGATTAAATGTCACAACTGAGCAATA 1532
QY 2636 ATATATTATTAATTTCACAAATTGAC 2661
DB 1533 ATATATTATTAATTTCACAAATTGAC 1558

RESULT 11
AAH06828
ID AAH06828 standard; cDNA; 816 BP.
AC AAH06828;
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:3663.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000BP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
PI Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR MPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
PS Claim 1; SEQ ID NO 3663; 2537bp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH1633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 816 BP; 182 A; 216 C; 253 G; 162 T; 0 U; 3 Other;
XX
Query Match 17.8%; Score 478; DB 4; Length 816;

Best Local Similarity 100.0%; Pred. No. 4,8e-167;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 GCCGCAATGCTCTTGAACAGCGCGCGCGAGCCGCTTCGGGTTCCGGCGGCGG 76
DB 5 GCCGCAATGCTCTTGAACAGCGCGCGCGAGCCGCTTCGGGTTCCGGGTTCCGGCGG 64
QY 77 GGAATGGAATCCCGAATGGAAGCGCGCGCGAGGAAGCAAGTCCCGCGCGCAACCTT 136
DB 65 GGAATGGAATCCCGAATGGAAGCGCGCGCGAGGAAGCAAGTCCCGCGCGCAACCTT 124
QY 137 GGGAGCGGCTCTGCTCTGCGCGCGAGGAGCGAGCGCGAGCTCTCTGAGGAAGC 196
DB 125 GGGAGCGGCTCTGCTCTGCGCGCGAGGAGCGAGCGCGAGCTCTCTGAGGAAGC 184
QY 197 GGGAGTGAACCATCGGCGCGAGAGCGAGTTGCGACCTTCTTCCCGCAATTAAC 256
DB 185 GGGAGTGAACCATCGGCGCGAGAGCGAGTTGCGACCTTCTTCCCGCAATTAAC 244
QY 257 TCTCTGGAATGCACTGTAGAAATTTGTAGTGAATGAATCAAGTCACTGAGCACTGGAAG 316
DB 245 TCTCTGGAATGCACTGTAGAAATTTGTAGTGAATGAATCAAGTCACTGAGCACTGGAAG 304
QY 317 ATACAGACACAGTGAACAGTGAATTAACAAGCTGAAGTTGTTAAGACAGACATGCC 376
DB 305 ATACAGACACAGTGAACAGTGAATTAACAAGCTGAAGTTGTTAAGACAGACATGCC 364
QY 377 CTTTACAGACTGGGAGTGTCTATCTTCTGTTACAGAAATGAACCGGAACACACAGC 436
DB 365 CTTTACAGACTGGGAGTGTCTATCTTCTGTTACAGAAATGAACCGGAACACACAGC 424
QY 437 TGGCATACCTCTATGAATCTTTAAGTGAAGAAAGCAAGCGATGACAAAGATCTTTGA 494
DB 425 TGGCATACCTCTATGAATCTTTAAGTGAAGAAAGCAAGCGATGACAAAGATCTTTGA 482

RESULT 12
AAH06846
ID AAH06846 standard; cDNA; 824 BP.
AC AAH06846;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:3681.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000BP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
PI Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR MPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
PT

PR		05-DEC-2000;	2000US-0251968P.	
PR		05-DEC-2000;	2000US-0256719P.	
PR		06-DEC-2000;	2000US-0251747P.	
PR		08-DEC-2000;	2000US-0251856P.	
PR		08-DEC-2000;	2000US-0251868P.	
PR		08-DEC-2000;	2000US-0251869P.	
PR		08-DEC-2000;	2000US-0251969P.	
PR		08-DEC-2000;	2000US-0251990P.	
PR		11-DEC-2000;	2000US-0254097P.	
PR		05-JAN-2001;	2001US-0259678P.	
XX				
PA	(HUMA-)	HUMAN GENOME SCI INC.		
PI	Rosen CA,	Barnaah SC,	Ruben SW;	
XX				
DR	WPI;	2001-468783/53.		
DR	P-PsDB;	MAUI6317.		
XX				
PT	New nucleic acid molecules encoding 461 human secreted proteins for			
PT	diagnosing, preventing, treating or ameliorating medical conditions and			
PT	used as food additives or preservatives.			
XX				
PS	Claim 1; SEQ ID NO 483; 980bp; English.			
CC	The invention relates to isolated nucleic acid molecules and their			
CC	encoded secreted proteins. The nucleic acids and proteins are used to			
CC	prevent, treat or ameliorate a medical condition in e.g. humans, mice,			
CC	rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used			
CC	in diagnosing a pathological condition or susceptibility to a			
CC	pathological condition. Antibodies to the proteins can also be used in			
CC	alleviating symptoms associated with the disorders and in diagnostic			
CC	immunoassays e.g. radiimmunoassays or enzyme linked immunosorbent assays			
CC	(ELISA). Disorders which are diagnosed or treated include autoimmune			
CC	diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.			
CC	neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac			
CC	arrest, cerebrovascular disorders e.g. cerebral ischemia, anglogenesis,			
CC	nervous system disorders e.g. Alzheimer's disease, infections caused by			
CC	bacteria, viruses and fungi and ocular disorders e.g. corneal infection,			
CC	and many other disorders listed in the specification. The polypeptides			
CC	can also be used to aid wound healing and epithelial cell proliferation,			
CC	to prevent skin aging due to sunburn, to maintain organs before			
CC	transplantation, for supporting cell culture of primary tissues, to			
CC	regenerate tissues and in chemotaxis. The polypeptides can also be used			
CC	as a food additive or preservative to increase or decrease storage			
CC	capabilities, fat content, lipid, protein, carbohydrate, vitamins,			
CC	minerals, cofactors and other nutritional components. The present			
CC	sequence encodes a novel secreted protein of the invention. Note: The			
CC	sequence data for this patent did not form part of the printed			
	Query March	17.0%; Score 455; DB 4; Length 693;		
	Best Local Similarity	100.0%; Pred. No. 1.6e-158; Mismatches	0; Gaps	0;
	Matches 455; Conservative	0; Indels	0;	
OY	1044 GCCCTGATGCACACGTTTCGGCGCGCTTGCTACTCGCGGTGATGAGCGCTTCTCCT			1103
Db	14 GCCTTGATGCACACGTTTCGGCGCGCTTGCTACTCGCGGTGATGAGCGCGCTTCTCCT			73
OY	1104 GTGTCTTAACCTGCCGCTGTCCCGTGAAGCGGATCTGTAAACAACCATCTCAACACT			1163
Db	74 GTGTCTTAACCTGCCGCTGTCCCGTGAAGCGGATCTGTAAACAACCATCTCAACACT			133
OY	1164 CGTGAAGCAATCTCTATCCAGATCCAGAACAAGTCGAGAGAAATAATGTGCAAG			1223
Db	134 CGTGAAGCAATCTCTATCCAGATCCAGAACAAGTCGAGAGAAATAATGTGCAAG			193
OY	1224 TATGATGCAAGAAATAATCACTCAAGACATGTCTCACCCCAAAGTCAGGCGGTCTTT			1283
Db	194 TATGATGCAAGAAATAATCACTCAAGACATGTCTCACCCCAAAGTCAGGCGGTCTTT			253
OY	1284 TTCTGATGAAGAAGAGATTCAAGAGACTCTTGAGACTGTCAAGACTTGACAGTAGTC			1343
Db	254 TTCTGATGAAGAAGAGAGATTCAAGAGACTCTTGAGACTGTCAAGACTTGACAGTAGTC			313

PT New nucleic acid molecules encoding 461 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 XX
 PS Claim 1, SEQ ID NO 483; 980bp; English.
 XX
 CC The invention relates to isolated nucleic acid molecules and their
 CC encoded secreted proteins. The nucleic acids and proteins are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Antibodies to the proteins can also be used in
 CC alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunoabsorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodenias,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
 CC and many other disorders listed in the specification. The polypeptides
 CC can also be used to aid wound healing and epithelial cell proliferation,
 CC to prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors and other nutritional components. The present
 CC sequence datafor this patent did not form part of the printed

Query Match	17.0%	Score 455;	DB 4;	Length 693;
Best Local Similarity	100.0%	Pred. No. 1.6e-158;		
Matches 455; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1044	GGCCGTGATGACAGCTTCTGCGGGCTTGCTACTCGGGGTGGATGGAAGGGCTGCTCT	1103
Db	14	GGCTTGATGACACGTTCTGCGGGCTTGCTACTCGGGGTGGATGGAAGGGCTGCTCT	73
QY	1104	GTCGTCCTACTGCGCGCTGTCCCGTGGAACGCGATCTGTAAACCAACATCTCTCAACACT	1163
Db	74	GTCGTCCTACTGCGCGCTGTCCCGTGGAACGCGATCTGTAAACCAACATCTCTCAACACT	133
QY	1164	CGTGGAGCATCTCTCATCCAGCATCCAGACAAAGGTGCGAGTGAAGAGATGTGCAAG	1223
Db	134	CGTGGAGCATCTCTCTCATCCAGCATCCAGACAAAGGTGCGAGTGAAGAGATGTGCAAG	193
QY	1224	TATGAGATGCCAGGATTAATACTCAAGCAGGTGCAAGCCCAAGTCAGGGGGCTTTT	1283
Db	194	TATGAGATGCCAGGATTAATACTCAAGCAGGTGCAAGCCCAAGTCAGGGGGCTTTT	253
QY	1284	TTCTGATGAAGAGGAGTTCAAGAGACTGCTGAGACTGTCAAGCGTTGACAGTGAATC	1343
Db	254	TTCTGATGAAGAGGAGTTCAAGAGACTGCTGAGACTGTCAAGCGTTGACAGTGAATC	313

PD 20-APR-2000.
XX
XX 15-OCT-1999; 99MO-US024206.
XX
XX 15-OCT-1998; 98US-0104436P.
XX
XX (GBMY) GENETICS INST INC.
XX
XX Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C,
XX Merberg D, Treacy M, Bowman MR;
XX WPI; 2000-317938/27.
XX
XX Isolated polynucleotides, and encoded proteins, comprising secreted
XX expressed sequence tags (ESTs), useful for treating various disorders
XX such as autoimmune, infectious, and central nervous system disorders.
XX
XX Claim 1; Page 437; 803pp; English.
XX
XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
XX sequence tags (ESTs), isolated from human, mouse, chicken and rat tissue
XX sources. The ESTs can have a range of activities depending on the
XX tissues they were isolated from. The activities include: chemotactic;
XX proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
XX haemostatic; thrombolytic; antiinflammatory; cyostatic; antibacterial;
XX antifungal; antiviral; antidiabetic; antistatic; vulnerary; antitumor;
XX osteoprotective; neuroprotective; nootropic; antiparkinsonian; antiproliferative;
XX cerebroprotective; anticonvulsant; and antidepressant. The ESTs can be
XX used for gene therapy and in vaccines. The ESTs are useful as probes for
XX the identification and isolation of full-length cDNAs and genomic DNA
XX molecules which correspond to the ESTs. Proteins encoded by the ESTs
XX are useful in assays for determining biological activity and raising
XX antibodies. They may be useful for treatment of autoimmune disorders
XX (multiple sclerosis, insulin dependent diabetes), allergic conditions
XX (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
XX osteoporosis, osteoarthritis, central nervous system disorders
XX (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
XX disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
XX disease), tumors, bacterial, fungal or viral infections, depression and
XX psoriasis. AAA45926 to AAA45931 represent linker variants which are given
XX in the exemplification of the present invention
XX
XX Sequence 575 BP; 124 A; 168 C; 165 G; 118 T; 0 U; 0 Other;
SQ
Query Match 10.7%; Score 286; DB 3; Length 575;
Best Local Similarity 100.0%; Pred. No. 5.6e-96;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 876 AGATGGAGACCTTGAACCTGAGCGGAGTGTGGTGGCAACCGCGTAAATGCCCA 935
DB 285 AGATGGAGACCTTGAACCTGAGCGGAGTGTGGTGGCAACCGCGTAAATGCCCA 344
QY 936 AACCGTCCAGAGAGCGTCAAGAGCAGCGGCTGGGAAACCAAGATGAGAGAGCGT 995
DB 345 AACCGTCCAGAGAGCGTCAAGAGCAGCGGCTGGGAAACCAAGATGAGAGAGCGT 404
QY 996 GACATGATCATCTGCGAGAGCCTGCTGACAGCATGCGCGTGAATTTGACGCTTCATGTA 1055
DB 405 GACATGATCATCTGCGAGAGCCTGCTGACAGCATGCGCGTGAATTTGACGCTTCATGTA 464
QY 1056 CACGTTCTCGCGGAGCTTGTACTCGGGCTGATGAGAGCGCTGTCCTGTCTTACCTG 1115
DB 465 CACGTTCTCGCGGAGCTTGTACTCGGGCTGATGAGAGCGCTGTCCTGTCTTACCTG 524
QY 1116 CCGCTGTCCCGTGGAGCGGATCTGTAAACCAATCTCAACAC 1161
DB 525 CCGCTGTCCCGTGGAGCGGATCTGTAAACCAATCTCAACAC 570
RESULT 17
AAS26143
ID AAS26143 standard; cDNA; 357 BP.
XX

AC AAS26143;
XX
XX 07-NOV-2001 (first entry)
XX
XX
XX
XX
XX Human cDNA encoding a novel secreted protein, Seq ID 322.
DE
XX
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic; cyostatic;
XX cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
XX antibacterial; vitruclide; fungicide; ophthalmological; vulnerary;
XX secreted protein; rheumatoid arthritis; hyperproliferative disorder;
XX cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
XX cerebral ischemia; angiogenesis; nervous system disorder;
XX Alzheimer's disease; infection; ocular disorder; corneal infection;
XX wound healing; epithelial cell proliferation; skin aging; food additive;
XX preservative; antiproliferative.
XX
XX Homo sapiens.
XX
XX WO200155322-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001MO-US001341.
XX
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
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XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
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XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226868P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227700P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 06-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX

QY 296 CAGGTGAGTGAACCTGAGATACCA 322
 DB 245 CAGGTGAGTGAACCTGAGATACCA 271

RESULT 18
 ABX73484
 ID ABX73484 standard; DNA; 357 BP.
 XX
 AC ABX73484;
 DT 18-MAR-2003 (first entry)
 XX
 DE Human novel polynucleotide #312.
 XX
 KM Human; gene; de; neural disorder; immune system disorder; renal disorder;
 KM muscular disorder; respiratory disease; reproductive disorder;
 KM gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KM hyperproliferative disorder; inflammatory disease; allergic reaction;
 KM blood related disorder; cancer; immunosuppressive; antiinflammatory;
 KM cardiovascular; nephrotoxic; cytostatic; antiallergic; thrombolytic;
 KM haemostatic; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN US2002132753-A1.
 PD 19-SEP-2002.
 XX
 PF 17-JAN-2001; 2001US-00764864.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225477P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
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 PR 29-SEP-2000; 2000US-0236369P.
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 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251855P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-147444/14.
 XX
 DR P-PSDB; ABUS5224.
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.
 XX
 PS Claim 1; SEQ ID NO 322; 402bp; English.
 XX
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
 CC human novel polynucleotides of the invention
 XX
 SQ Sequence 357 BP; 84 A; 87 C; 118 G; 66 T; 0 U; 2 Other;

Query Match 10.0%; Score 267; DB 8; Length 357;
 Best Local Similarity 100.0%; Pred. No. 6; Se-89;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 TCCGGGTTCCGCGCGCGGCGGAGTGTGAATCCGATGAGCGGCGGAGGAGCAAGC 115
 DB 5 TCCGGGTTCCGCGCGCGGCGGAGTGTGAATCCGATGAGCGGCGGAGGAGCAAGC 64

QY 116 AGTCGCGCGCGCGCGAGCCTTGAGGACGCGCTCTGCGCTTGAGGCGCGGAGGAGCGGAGC 175
 DB 65 AGTCGCGCGCGCGCGAGCCTTGAGGACGCGCTCTGCGCTTGAGGCGCGGAGGAGCGGAGC 124

QY 176 CGCAGCTCTCTCTAGAGAGAGGAGAGTGCATCCATCGGCGGAGAGCAGAGTTGCCACTTT 235
 DB 125 CGCAGCTCTCTCTAGAGAGAGGAGAGTGCATCCATCGGCGGAGAGCAGAGTTGCCACTTT 184

QY 236 CTTTCCCGCAGCAATAAATCTGTCTGTGAGATCACTGTAGATTTGTAGTGAATAAAT 295
 DB 185 CTTTCCCGCAGCAATAAATCTGTCTGTGAGATCACTGTAGATTTGTAGTGAATAAAT 244

QY 296 CAGGTGAGTGAACCTGAGATACCA 322
 DB 245 CAGGTGAGTGAACCTGAGATACCA 271

RESULT 19
 AAS26563
 ID AAS26563 standard; CDNA; 354 BP.
 XX
 AC AAS26563;

XX 07-NOV-2001 (first entry)
DT Human cDNA encoding a novel secreted protein, Seq ID 742.
XX
DE
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virocidic; fungicide; ophthalmological; vulnery;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155322-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001341.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
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PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
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PR 05-SEP-2000; 2000US-0229513P.
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PR 08-SEP-2000; 2000US-0232080P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
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PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249399P.
PR 17-NOV-2000; 2000US-0249399P.
PR 17-NOV-2000; 2000US-0249399P.

PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251888P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-488783/53.
XX P-PSDB; AAU16576.
DR
DR
XX
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX
PS Claim 1; SEQ ID NO 742; 980pp; English.

XX
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC immunosays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed

Query Match 8.9%; Score 238; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 3.5e-78;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GCATTAATGCTGCTCTGAGATCACTGTAAGTGTGATGTAAGTAAGTCAAGTCAAG 304
DB 51 GCATTAATGCTGCTCTGAGATCACTGTAAGTGTGATGTAAGTCAAGTCAAGTCAAG 110
QY 305 TGACATGGAATGACAGACAGCAGTGAAGAGTGAATTAAGAAAGTGAAGTGTGAAGA 364
DB 111 TGACATGGAATGACAGACAGCAGTGAAGAGTGAATTAAGAAAGTGAAGTGTGAAGA 170
QY 365 AGCAGATGACCTCTTACAGACTGGGAGTGTATCTACTTGTGTGTAAGTAAGTAAGAC 424
DB 171 AGCAGATGACCTCTTACAGACTGGGAGTGTATCTACTTGTGTGTAAGTAAGTAAGAC 230
QY 425 CGGAACACAGCTGGGATGCTCTTATGAATCTTTTAAGTAAGTAAGTAAGTAAGTAAGAC 482
DB 231 CGGAACACAGCTGGGATGCTCTTATGAATCTTTTAAGTAAGTAAGTAAGTAAGTAAGAC 288

RESULT 20
AAS26144
ID AAS26144 standard; cDNA; 354 BP.
XX
XX
AC AAS26144;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, Seq ID 323.
XX
XX
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cyrostatic;
KW cardiact; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; optalmallogical; vulnerary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiodysplasia; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
XX
OS Homo sapiens.
XX
XX
PN WO20015322-A2.
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US001341.
XX
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184668P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
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PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.

PA (DBMA/) DRMANAC R T.
PA (LABA/) LABAT I. I.
PA (STRC/) STRACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Strache-Crain B, Dickson MC, Jones LW,
XX
DR WPI, 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
PS Claim 1; SEQ ID NO 13662; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridization). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations,
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 449 BP; 147 A; 76 C; 86 G; 135 T; 0 U; 5 Other;
Query Match 8.1%; Score 217; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 2e-70; 0; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0;
QY 2445 AGTTCAAGGAGAGAGGAGGAGTTTATCAAAAACATTTGTCAGAGAGGAGCATAG 2504
DB 92 AGTTCAAGGAGAGAGGAGGAGGAGTTTATCAAAAACATTTGTCAGAGAGGAGCATAG 151
QY 2505 TTTCAGCCTACAGAGAGGAGGAGGAGTTTATCAAAAACATTTGTCAGAGAGGAGCATAG 2564
DB 152 TTTCAGCCTACAGAGAGGAGGAGGAGTTTATCAAAAACATTTGTCAGAGAGGAGCATAG 211
QY 2565 ATTTTATTTATTTATGTTGTTGTTATCTTTCTTAATGAATTTAATGTCACAACTG 2624
DB 212 ATTTTATTTATTTAATGTTGTTGTTATCTTTCTTAATGAATTTAATGTCACAACTG 271
QY 2625 TAGCAAAATATATATATTTATTTATTTAATGTCACAACTG 2661
DB 272 TAGCAAAATATATATTTATTTATTTAATGTCACAACTG 308
RESULT 24
ABAI6633
ID ABAI6633 standard; DNA; 13836 BP.
XX
XX ABAI6633;
AC
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 8964.
XX
XX Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischistosomal; antianemic; antitachycardic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;

KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX Homo sapiens.
XX WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 19-MAY-2000; 2000US-0205515P.
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PR 28-JUN-2000; 2000US-0214865P.
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PR 14-AUG-2000; 2000US-0225758P.
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PR 18-AUG-2000; 2000US-0226279P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 12-SEP-2000; 2000US-0231966P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 21-SEP-2000; 2000US-0234274P.

PR	25-SEP-2000	2000US-02349987P
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PR	27-SEP-2000	2000US-02350834P
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PR	20-OCT-2000	2000US-02417855P
PR	20-OCT-2000	2000US-02417866P
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PR	01-NOV-2000	2000US-02464177P
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PR	08-NOV-2000	2000US-02465524P
PR	08-NOV-2000	2000US-02465525P
PR	08-NOV-2000	2000US-02465525P
PR	08-NOV-2000	2000US-02465577P
PR	08-NOV-2000	2000US-02465577P
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PR	08-NOV-2000	2000US-02465588P
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PR	08-NOV-2000	2000US-02466110P
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PR	17-NOV-2000	2000US-02492077P
PR	17-NOV-2000	2000US-02492088P
PR	17-NOV-2000	2000US-02492088P
PR	17-NOV-2000	2000US-02492099P
PR	17-NOV-2000	2000US-02492099P
PR	17-NOV-2000	2000US-02492100P
PR	17-NOV-2000	2000US-02492100P
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PR	17-NOV-2000	2000US-02492112P
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PR	17-NOV-2000	2000US-02492133P
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PR	17-NOV-2000	2000US-02492151P
PR	17-NOV-2000	2000US-02492151P
PR	17-NOV-2000	2000US-02492165P
PR	17-NOV-2000	2000US-02492165P
PR	17-NOV-2000	2000US-02492177P
PR	17-NOV-2000	2000US-02492177P
PR	17-NOV-2000	2000US-02492188P
PR	17-NOV-2000	2000US-02492188P
PR	17-NOV-2000	2000US-02492244P
PR	17-NOV-2000	2000US-02492244P
PR	17-NOV-2000	2000US-02492245P
PR	17-NOV-2000	2000US-02492245P
PR	17-NOV-2000	2000US-02492265P
PR	17-NOV-2000	2000US-02492265P
PR	17-NOV-2000	2000US-02510300P
PR	17-NOV-2000	2000US-02510300P
PR	17-NOV-2000	2000US-02493300P
PR	17-NOV-2000	2000US-02493300P
PR	01-DEC-2000	2000US-02503911P
PR	01-DEC-2000	2000US-02503911P
PR	01-DEC-2000	2000US-02511606P
PR	01-DEC-2000	2000US-02511606P
PR	08-DEC-2000	2000US-02518689P
PR	08-DEC-2000	2000US-02518689P
PR	08-DEC-2000	2000US-02519898P
PR	08-DEC-2000	2000US-02519898P
PR	11-DEC-2000	2000US-02519900P
PR	11-DEC-2000	2000US-02519900P

PR	05-JAN-2001; 2001US-0259678P.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
PI	Rosen CA, Barash SC, Ruben SW;
XX	WPI; 2001-541565/60.
DR	
XX	Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT	useful for preventing, diagnosing and/or treating nervous system cancers
PR	and metastases.
PS	Disclosure; SEQ ID NO 8964; 1701bp + Sequence listing; English.
XX	
CC	The invention relates to novel genes (ABAI1004-ABA21534) and proteins
CC	(ABBI4678-ABBI18001) useful for preventing, treating or ameliorating
CC	medical conditions e.g. by protein or gene therapy. The genes are
CC	isolated from a range of human tissues disclosed in the specification.
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC	the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC	ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC	breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC	disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC	anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC	multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC	cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC	; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC	infectious diseases such as viral, bacterial, fungal and parasitic
CC	infections. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 13836 BP; 3132 A; 3517 C; 3683 G; 3504 T; 0 U; 0 Other;
Query Match	6.3%; Score 169; DB 5; Length 13836;
Best Local Similarity	100.0%; Pred. No. 6.7e-53;
Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	709 GGGTCTGGGCGGTGTGGCATCTCCCTTAAGGAAGTGTCCTCTGTGGCAAGTATGAA 768
DB	266 GGGTCTGGGCGGTGTGGCATCTCCCTTAAGGAAGTGTCCTCTGTGGCAAGTATGAA 325
QY	769 GTCTCAGCTTTGCCCTCAGACTTCCCAGAACAAGACTGCCTCTTTGCGTTGCAA 828
DB	326 GTCTCAGCTTTGCCCTCAGACTTCCCAGAACAAGACTGCCTCTTTGCGTTGCAA 385
QY	829 CCCGACGATCCAGAGATTGGAGCCCGTGAAGAAATGAGAGAG 877
DB	386 CCCGACGATCCAGAGATTGGAGCCCGTGAAGAAATGAGAGAG 434
RESULT 25	
AIDS8374	ID AAKS8374 standard; CDNA; 825 BP.
XX	
AC	AAKS8374;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3434.
XX	
KM	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX	cyclostatic; gene therapy; vaccine; metaasts; ss.
OS	Homo sapiens.
XX	
PN	WO200157182-A2.
XX	
PD	09-AUG-2001.
PF	17-JAN-2001; 2001WO-US001354.
XX	
PR	31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
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PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
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PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0232196P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234979P.
PR 25-SEP-2000; 2000US-0234986P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251986P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI, 2001-483426/52.
XX P-PSDB; AAM85593.
DR
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX

PS Claim 1; SEQ ID NO 3434; 3071bp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 825 BP; 216 A; 187 C; 206 G; 209 T; 0 U; 7 Other;
Query Match 5.2%; Score 139; DB 4; Length 825;
Best Local Similarity 99.5%; Pred. No. 1.3e-41;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1702 GAGCTCAACCTGGGTGACAAAGTGTCTGAGCGGCTGTGAAACAACAGCTACGATCA 1761
DB 348 GAGCTCAACCTGGGTGACAAAGTGTCTGAGCGGCTGTGAAACAACAGCTACGATCA 407
QY 1762 GACATCCTGAAGATTACCTGGCAACGAGGTTTGACATGAAAAACATGTTGACCGAG 1821
DB 408 GACATCCTGAAGATTACCTGGCAACGAGGTTTGACATGAAAAACATGTTGACCGAG 467
QY 1822 AGCCTCGTGGCTCTCCAGCGGAGAGTGTCTGCTGCTGATTACAGAGTCAAGGAGAC 1881
DB 468 AGCCTCGTGGCTCTCCAGCGGAGAGTGTCTGCTGCTGATTACAGAGTCAAGGAGAC 527
QY 1882 ACCGTTCTGT 1891
DB 528 ACCGTTCTGT 537
RESULT 26
ABN60913/C
ID ABN60913 standard; cDNA; 617 BP.
AC ABN60913;
XX
XX 28-JUN-2002 (first entry)
DE Human cancer related polynucleotide SEQ ID NO 880.
XX
XX Human; cytostatic; gene expression; gene mapping; tissue profiling;
KW gene therapy; cancer; tumour; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200214500-A2.
XX
XX 21-FEB-2002.
XX
XX 16-AUG-2001; 2001MO-US05840.
XX
XX 16-AUG-2000; 2000US-0226326P.
XX
XX (CHIR) CHIRON CORP.
XX (HYSR-) HYSRQ INC.
XX
XX Sacobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F,
PI Lamson G, Scott EM, Zhang G, Kaessam A, Pot D, Labat I;
XX
XX WPI; 2002-241905/29.

XX
XX New nucleic acid for producing a polypeptide, detecting differentially
PT expressed genes correlated with a cancerous state of a mammalian cell,
PT and inhibiting tumor growth.
XX
XX
XX Claim 1; SEQ ID NO 880; 883bp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
CC with cytostatic activity. The polynucleotide is used to produce a
CC polypeptide, to detect differentially expressed genes correlated with a
CC cancerous state of a mammalian cell and to inhibit tumour growth. The
CC polynucleotide is used as a probe in mapping and tissue profiling. The
CC encoded polypeptide and antibodies to the polypeptide can also be used
CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
CC gene therapy. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 617 BP; 181 A; 155 C; 159 G; 122 T; 0 U; 0 Other;
Query Match 2.9%; Score 78; DB 6; Length 617;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1966 CCAGTGGCCGTAACTCCGCTGCTGACTGCTGAGGCGCGTAAGTCCGCACTCAGGTG 2025
DB 385 CCAGTGGCCGTAACTCCGCTGCTGACTGCTGAGGCGCGTAAGTCCGCACTCAGGTG 326
QY 2026 AAAGCTCACACAGCCATG 2043
DB 325 AAAGCTCACACAGCCATG 308
RESULT 27
ACH14968
ID ACH14968 standard; cDNA; 476 BP.
XX
XX ACH14968;
AC ACH14968;
XX
XX 13-OCT-2003 (first entry)
DE Human adult brain cDNA #2180.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 2180; 44bp; English.
XX

CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome.
CC In forensic, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
CC
XX
SQ Sequence 476 BP; 114 A; 112 C; 135 G; 106 T; 0 U; 9 Other;
Query Match 2.9%; Score 77; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.2e-18;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2046 ATTCAATCATATCTGTGGAACAGACAGGTTCAAAACTAAGCATCCAGAGCCCTGAGCA 2105
DB 52 ATTCAATCATATCTGTGGAACAGACAGGTTCAAAACTAAGCATCCAGAGCCCTGAGCA 111
QY 2106 GCTTTCAGCACTGAGG 2122
DB 112 GCTTTCAGCACTGAGG 128
RESULT 28
ID ABN33472
ID ABN33472 standard; DNA; 60 BP.
AC ABN33472;
XX
DT 15-JUL-2002 (first entry)
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6220.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN MO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Maeserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 6220; 47bp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
CC
XX
SQ Sequence 60 BP; 10 A; 12 C; 18 G; 20 T; 0 U; 0 Other;
Query Match 2.2%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1843 GGAGTGTTCCTGCTGTGATTACAGAGTCAACGGAGACACCGTTCTGTACTGCTGT 1902
DB 1 GGAGTGTTCCTGCTGTGATTACAGAGTCAACGGAGACACCGTTCTGTACTGCTGT 60
RESULT 29
ID AAQ22007/C
ID AAQ22007 standard; DNA; 860 BP.
AC AAQ22007;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 09-JUN-1992 (first entry)
XX
DE Sequence encoding Cor a I allergen of hazel.
XX
KW Fagales; hazel; IGB; tree allergen; pollen; antibodies; T-cell response;
KW ss.
XX
OS Fagales.
XX
OS
XX
FH Key
FH CDS
FT 1..483
FT /*tag= a
FT /product= "Aln_g_I"
FT 846..860
FT /*tag= b
XX
PN WO9202621-A.
XX
PD 20-FEB-1992.
XX
PF 08-AUG-1990; 90AT-00001668.
XX
PR 08-AUG-1990; 90AT-00001668.
PR 11-APR-1991; 91US-00683831.
XX
PA (BIOM-) BIOMAY BIOTECHN PRO.
XX
PI Beltenede H, Reikersfor A, Valenta R, Hoffmannso K, Breitenbac M;
XX
PI Kraft D, Rumpold H, Scheiner O;
XX
DR WPI; 1992-080075/10.
DR P-PsDB; AAR21795.
XX

PT Aln g I, Cor a I and Bet v I allergens - and DNA from alder, hazel and
 XX birch, useful in diagnosis or therapy of allergic diseases.
 XX
 PS Claim 8; Page 36; 54pp; English.
 CC The cDNA sequence encoding the Cor a I allergen of hazel was obtd. from
 CC the polyA+ mRNA isolated from ripe hazel pollen. The resulting cDNA was
 CC amplified by PCR using primers whose sequences were derived from the N-
 CC terminal amino-acid sequence of Cor a I. The DNA fragment produced was
 CC cloned into the pBluescript KS vector and transformed into E. coli XL1-
 CC Blue cells. The sequence allows mammals to be tested for allergic
 CC reactions to specific tree allergens. The derived polypeptide may be used
 CC to challenge the mammal to elicit bronchial, conjunctival, dermal, nasal
 CC or oral provocation. The polypeptide may be used to treat a mammal
 CC afflicted with a pollen allergy. It is administered in an amount
 CC sufficient to hypersensitize the mammal to Cor a I. See also AA022001-8
 CC and AA021974. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
 CC 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 860 BP; 274 A; 150 C; 190 G; 246 T; 0 U; 0 Other;
 Query Match 1.0%; Score 26; DB 2; Length 860;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2654 AATTCGCAAAAAAAAAAAAAAAAAA 2679
 DB 754 AATTCGCAAAAAAAAAAAAAAAAAA 729
 RESULT 30
 ADF45549/C
 ID ADF45549 standard; DNA; 1000 BP.
 XX
 AC ADF45549;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Arabidopsis thaliana disease stress responsive promoter SEQ ID NO:18.
 XX
 KW promoter; disease stress-responsive promoter; stress resistance; plant;
 KM Alternaria brassicicola infection; infection;
 XX disease stress resistant plant; Arabidopsis thaliana, ds.
 OS Arabidopsis thaliana.
 XX
 PN JP2003284566-A.
 XX
 PD 07-OCT-2003.
 XX
 PF 29-MAR-2002; 2002JP-00095389.
 XX
 PR 29-MAR-2002; 2002JP-00095389.
 XX
 PA (RIKA) RIKAGAKU KENKUSHO.
 XX
 DR WPI; 2003-885429/82.
 XX
 PT Novel stress-responsive promoter useful for producing disease stress
 PT resistant plants, for elucidating disease stress resistance response in
 PT plant.
 PS Claim 1; SEQ ID NO 18; 24pp; Japanese.
 XX
 CC The present invention describes a promoter (I) comprising DNA having any
 CC one of 21 1000-nucleotide long sequences (S1, see ADF45532 to ADF45552),
 CC DNA having nucleotides in which one or more of nucleotides of (S1) is
 CC deleted, substituted or added and functions as disease stress-responsive
 CC promoter (DP), and DNA which hybridizes with (S1) and functions as DP.
 CC Also described: (1) an expression vector (II) comprising (I); (2) a
 CC transformed organism (III) comprising (II); and (3) producing stress
 CC resistant plant by (III). (I) responds to disease stress, where the

CC stress is caused by black sooty-mould microbe (Alternaria brassicicola)
 CC infection. (III) is useful for producing a transgenic plant. (I) is
 CC useful for producing a disease stress resistant plant and for elucidating
 CC the disease stress resistance response in plant. (I) enables the
 CC detection of stress caused by A. brassicicola infection. The present
 CC sequence represents an Arabidopsis thaliana disease stress-responsive
 CC promoter sequence, which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 1000 BP; 331 A; 162 C; 138 G; 369 T; 0 U; 0 Other;
 Query Match 0.9%; Score 25; DB 10; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2655 AATTGACAAAAAAAAAAAAAAAAA 2679
 DB 285 AATTGACAAAAAAAAAAAAAAAAA 261
 RESULT 31
 AAA96229
 ID AAA96229 standard; cDNA; 1085 BP.
 XX
 AC AAA96229;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE cDNA encoding a maize chitinase polypeptide designated ZmCh13.
 XX
 KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;
 KM pathogen control; disease resistance; molecular marker; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 46..969
 FT /*tag= a
 FT /product= "chitinase"
 XX
 PN WO200056908-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 09-MAR-2000; 2000MO-US006121.
 XX
 PR 24-MAR-1999; 99US-0125915P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Simmons CR, Valpani N;
 XX
 DR WPI; 2000-628269/60.
 XX
 DR P-PSDB; AAB18901.
 XX
 PT New maize chitinase genes encoding seven chitinases of glucosyl hydrolase
 PT family 19 are useful for enhancing disease resistance in crop plants by
 PT modulating its expression in plants.
 XX
 PS Claim 1; Page 79-81; 96pp; English.
 XX
 CC The present sequence encodes a chitinase polypeptide. The specification
 CC describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896,
 CC AAB18899, and AAB18902-05), and glucosyl hydrolase family 18 chitinases
 CC (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants
 CC can be modulated to enhance disease resistance in crop plants and for
 CC control of pathogens. The chitinase polynucleotides are also useful as
 CC molecular markers for genotype in a plant, and for sequence shuffling
 XX
 SQ Sequence 1085 BP; 208 A; 391 C; 330 G; 156 T; 0 U; 0 Other;
 Query Match 0.9%; Score 25; DB 3; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 19;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAA 2679
 1061 AATTGACAAAAA 1085

RESULT 32
 AAD39143
 ID AAD39143 standard; cDNA; 1963 BP.
 XX
 AC AAD39143;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human transporter-2 (TP-2) cDNA, 63760.
 XX
 KW Human; 63760 protein; transporter-2; TP-2; drug screening; gene therapy;
 KW pharmacogenetics; central nervous system; Alzheimer's disease; epilepsy;
 KW senile dementia; depression; cardiac related disorder; arteriosclerosis;
 KW restenosis; myocardial infarction; cancer; cell differentiation; growth;
 KW hormonal disorder; pituitary; thyroid; hyperthyroidism; hypothyroidism;
 KW immune; transient hypogammaglobulinaemia; immunostimulator; anorectic;
 KW congenital X-linked infantile hypogammaglobulinaemia; sugar homeostasis;
 KW anorexia; neuroprotective; antiarteriosclerotic; cardiac; cytosstatic;
 KW antidepressant; vasotropic; anticonvulsant; nootropic; metabolic;
 KW obesity; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 67..1491
 FT /tag= a
 FT /product= "Human transporter-2 (TP-2) protein"
 XX
 MO200224911-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 19-SEP-2001; 2001WO-US029373.
 XX
 PR 19-SEP-2000; 2000US-0233790P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2002-479523/51.
 DR P-PSDB; AAE24349.
 XX
 PT Novel human transporter 2 polypeptide referred as 63760 polypeptide which
 PT is a member of human transporter family, useful as reagents or targets
 PT for treating TP-2 mediated disorders such as senile dementia, depression.
 XX
 PS Claim 1; Fig 1; 96pp; English.
 XX
 CC The invention relates to 63760 polypeptide (a human transporter family
 CC member, referred to as transporter-2 (TP-2)) and its corresponding
 CC nucleic acid. 63760 protein is useful for treating disorders
 CC characterised by insufficient or excessive production of a 63760
 CC substrate or for producing 63760 inhibitors, screening for drugs or
 CC compounds which modulate 63760 activity. 63760 DNA is used in gene
 CC therapy. 63760 protein, DNA and its antibody are useful for screening
 CC assays, predictive medicine (e.g., diagnostic assays, prognostic assays,
 CC monitoring clinical trials, and pharmacogenetics); and methods of
 CC treatment (e.g., therapeutic and prophylactic). 63760 protein, DNA and
 CC its antibody are useful as a novel diagnostic target and therapeutic
 CC agent in assays applicable to treatment and diagnosis of 63760 mediated
 CC or related disorders including central nervous system disorders such as
 CC Alzheimer's disease, senile dementia, epilepsy, depression, etc; cardiac
 CC related disorders such as arteriosclerosis, restenosis, myocardial
 CC infarction, etc; cancer by modulating cellular growth, differentiation or
 CC migration; hormonal disorders such as pituitary disorders (growth

CC disorders), thyroid disorders (hyperthyroidism, hypothyroidism), etc;
 CC immune disorder such as transient hypogammaglobulinaemia, congenital X-
 CC linked, infantile hypogammaglobulinaemia, etc; disorders associated with
 CC sugar homeostasis such as obesity, anorexia, etc. The 63760 molecules are
 CC useful as surrogate markers for one or more disorders or disease states
 CC or for conditions leading up to disease states, as pharmacodynamic
 CC markers and as pharmacogenomic markers. The present sequence is human TP-
 CC 2 cDNA
 XX
 SQ Sequence 1963 BP; 426 A; 505 C; 562 G; 470 T; 0 U; 0 Other;
 XX
 Query Match 0.9%; Score 25; DB 6; Length 1963;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAA 2679
 1916 AATTGACAAAAA 1940

RESULT 33
 AAD37442
 ID AAD37442 standard; cDNA; 1963 BP.
 XX
 AC AAD37442;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human transporter TP2 cDNA #1.
 XX
 KW Human; ss; gene; transporter; cytosstatic; anorectic; antidiabetic;
 KW anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour;
 KW obesity; epilepsy; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN US2003143675-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 22-MAY-2002; 2002US-00154419.
 XX
 PR 12-MAY-2000; 2000US-0204211P.
 PR 29-JUN-2000; 2000US-0215376P.
 PR 31-JUL-2000; 2000US-0221769P.
 PR 19-SEP-2000; 2000US-0233790P.
 PR 25-SEP-2000; 2000US-0235107P.
 PR 05-OCT-2000; 2000US-0238336P.
 PR 14-NOV-2000; 2000US-0248364P.
 PR 15-NOV-2000; 2000US-0248878P.
 PR 15-DEC-2000; 2000US-0256240P.
 PR 18-DEC-2000; 2000US-0256588P.
 PR 21-DEC-2000; 2000US-0258028P.
 PR 22-JAN-2001; 2001US-0263169P.
 PR 14-MAY-2001; 2001US-00858194.
 PR 29-JUN-2001; 2001US-00858111.
 PR 31-JUL-2001; 2001US-00919781.
 PR 19-SEP-2001; 2001US-00957664.
 PR 25-SEP-2001; 2001US-00964295.
 PR 05-OCT-2001; 2001US-00972724.
 PR 14-NOV-2001; 2001US-00002762.
 PR 17-DEC-2001; 2001US-00024623.
 PR 22-JAN-2002; 2002US-00055025.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ, Glucksmann MA, Meyers RE;
 XX
 DR WPI; 2003-851783/79.
 DR P-PSDB; AAD37443.
 XX
 PT New isolated nucleic acid, useful for preparing a composition for
 PT treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy

PT or diabetes.
XX
PS Claim 1; SEQ ID NO 15; 663bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a cDNA
CC encoding a human transporter protein, or its complement, a sequence that
CC is 60 % identical to the cDNA, a fragment comprising at least 30
CC nucleotides of the cDNA, or a sequence encoding a fragment of the
CC polypeptide comprising at least 10 contiguous amino acid residues of the
CC cDNA. Also included are a vector comprising the novel nucleic acid
CC molecule, producing the polypeptide, the isolated transporter
CC polypeptide, an isolated antibody that specifically binds to the
CC polypeptide, detecting the presence of the polypeptide or nucleic acid in
CC a sample, a kit, identifying a compound that binds to, or that modulates
CC the activity of, the polypeptide, and modulating the activity of the
CC polypeptide. The nucleic acid is useful for preparing a composition for
CC treating PCG-1 (not defined) associated disorders e.g. liver tumours,
CC obesity, epilepsy or diabetes. The present sequence encodes a novel human
CC transporter protein.
XX
SQ Sequence 1963 BP; 426 A; 505 C; 562 G; 470 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 25; DB 10; Length 1963;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2655 AATTGACAAAAA 2679
DB 1916 AATTGACAAAAA 1940
RESULT 34
AB215532/C
ID AB215532 standard; DNA; 2000 BP.
XX
AC AB215532;
XX
XX 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3337.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
XX 28-FEB-2002.
XX
PD 24-AUG-2001; 2001WO-US026685.
XX
PF 24-AUG-2000; 2000US-0227866P.
XX
PR 26-JAN-2001; 2001US-0264647P.
XX
PR 22-JUN-2001; 2001US-0300111P.
XX
XX
PA (SCRI) SCRIPPS RES INST.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
XX
PI MPI; 2002-304127/34.
XX
DR Identifying a stress condition to which a plant cell has been exposed and
XX
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 3337; 577bp + Sequence Listing; English.
XX
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the .

CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB215532) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2000 BP; 733 A; 326 C; 269 G; 672 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 25; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2655 AATTGACAAAAA 2679
DB 1268 AATTGACAAAAA 1244
RESULT 35
ADA69051/C
ID ADA69051 standard; DNA; 2000 BP.
XX
AC ADA69051;
XX
XX 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 2374.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
PD 22-JUN-2001; 2001WO-IB001105.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX
PI Katsirli F, Qian S, Tao Y, Whitam S, Xie Z, Zhu T, Zou G;
XX
DR MPI; 2003-175290/17.
XX
XX
PT Identifying at least one gene involved in plant resistance or response to
XX
PT pathogenic infection for conferring resistance or tolerance to a plant to
XX
PT bacterial, fungal or viral infection by determining or detecting plant
XX
PT gene expression.
XX
PS Claim 27; SEQ ID NO 2374; 899bp; English.
XX
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC the expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 733 A; 326 C; 269 G; 672 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 25; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2655 AATTGACAAAAA 2679

XX (CORI-) CORIXA CORP.
XX Algate PA, Harlocker SL, Jones R;
XX WPI; 2002-122075/16.
XX
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX
XX Claim 1, SEQ ID NO 9622; 489pp; English.
XX
XX The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumor
CC polypeptide encoded by a polynucleotide (III) having a CDNA sequence (SI)
CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
CC or antigen presenting cells that express (II), (I) has cytostatic
CC activity. An oligonucleotide (IV) that hybridises to (SI) can be used for
CC detecting ovarian cancer in a patient's biological sample preferably
CC serum or ovarian tissue. The method comprises contacting a biological
CC sample from a patient with (IV), detecting the amount of polynucleotide
CC hybridising to (IV) and comparing the amount to a predetermined cutoff
CC value and thereby detecting ovarian cancer in the patient, where the
CC amount of polynucleotide hybridising to (IV) is detected preferably by
CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC useful for stimulating and/or expanding T cells specific for an ovarian
CC tumor protein comprising contacting T cells with (III) or (II). (III) is
CC useful in design and preparation of ribozyme molecules for inhibiting
CC expression of the tumor polypeptides and proteins in tumour cells; and
CC to isolate a full length gene from a suitable library e.g., a tumour CDNA
CC library using well known techniques
XX
SQ Sequence 199 BP; 81 A; 36 C; 49 G; 33 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 24; DB 6; Length 199;
Best Local Similarity: 100.0%; Pred. No. 58;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2656 ATTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 160 ATTGACAAAAAAAAAAAAAAAAAAAA 183
RESULT 39
AAS29141
ID AAS29141 standard; CDNA; 222 BP.
XX
XX AAS29141;
AC
XX 21-NOV-2001 (first entry)
DT
XX
XX
DE CDNA encoding for human DNA-binding protein #112.
XX
XX
XX Human; DNA-binding protein; histone; chromo domain protein;
KW chromatin organisation modifier; Y-box binding protein; DNA organisation;
KW gene transcription; malignant disease; autoimmune disorder;
KW rheumatic disease; genetic abnormality; infectious disease;
KW neurological disorder; gene therapy; immunomodulatory; anti-HIV;
KW anti rheumatic; anti microbial; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200155162-A1.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001MO-US001305.
PF
XX
XX 31-JAN-2000; 2000US-0179065P.
PR
XX 04-FEB-2000; 2000US-0180628P.
PR

PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 14-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 05-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.

PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236882P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241211P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251889P.
 PR 08-DEC-2000; 2000US-0251909P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Barash SC, Ruben SM,
 XX
 DR WPI; 2001-465557/50.
 XX P-PSDB; AAU18193.
 PT
 PT Nucleic acid molecules encoding human secreted chromosomal binding
 PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
 XX Alzheimer's and Parkinson's diseases and cancers.
 XX
 XX
 XX Claim 4; SEQ ID NO 50; 561pp; English.
 CC The present invention relates to the isolation of novel DNA-binding
 CC proteins (AAU1814-AAU1821), and cDNA and genomic sequences encoding for
 CC these proteins. DNA-binding proteins such as histones, chromo (chromatin
 CC organisation modifier) domain proteins, and Y-box binding proteins may
 CC contribute to diseases resulting from aberrant DNA organisation and/or
 CC gene transcription. The sequences of the invention are useful in
 CC screening assays to identify antagonists and/or agonists that may enhance
 CC or block activities mediated by DNA-binding proteins. Blockers of DNA-
 CC binding proteins may be useful in treating disorders such as malignant
 CC diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus),
 CC rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities
 CC (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological

CC disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the
CC invention may also be used in gene therapy. AAS29030-AAS29157 represent
CC cDNA sequences encoding for novel DNA-binding proteins. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 222 BP; 112 A; 26 C; 25 G; 57 T; 0 U; 2 Other;

Query Match 0.9%; Score 24; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 145 ATTGACAAAAA 168

RESULT 41
ABS68281
ID ABS68281 standard; cDNA; 222 BP.
XX
AC ABS68281;
XX
DT 18-NOV-2002 (first entry)
XX
DE cDNA encoding human DNA-binding protein #112.
XX
KW Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder;
KW severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease;
KW diabetes mellitus; allergy; ashma; inflammatory condition; thrombosis;
KW graft-versus-host disease; blood-related disorder; atherosclerosis;
KW hyperproliferative disorder; cancer; renal disorder; arrhythmia;
KW acute glomerulonephritis; cardiovascular disorder; respiratory disorder;
KW Goodpasture's syndrome; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; endocrine disorder; Addison's disease; gene;
KW reproductive system disorder; endometriosis; infectious disease;
KW viral infection; bacterial infection; fungal infection; vaccine;
KW gastrointestinal disorder; multiple sclerosis; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN US2002102638-A1.
XX
PD 01-AUG-2002.
XX
PF 17-JAN-2001; 2001US-00764846.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216880P.
PR 14-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 26-JUL-2000; 2000US-0220863P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 22-AUG-2000; 2000US-0225758P.
PR 30-AUG-2000; 2000US-0226868P.
PR 01-SEP-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
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PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI, 2002-690611/74.
XX P-PSDB; ABG92686.
XX
XX
XX Novel DNA-binding protein useful for diagnosis, prognosis, prevention and
XX treatment of immune, hyperproliferative, respiratory, cardiovascular,
XX reproductive, endocrine, gastrointestinal and neurological disorders.
XX
XX
XX Claim 1; SEQ ID NO 122; 225bp; English.

XX
XX
XX The present invention relates to a new DNA-binding protein. The invention
XX is useful in treating, preventing, diagnosing and/or prognosing
XX immunodeficiencies (e.g. B cell immunodeficiencies, severe combined
XX immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple
XX sclerosis, diabetes mellitus), allergic reactions and conditions (e.g.
XX asthma), inflammatory conditions, graft-versus-host disease, blood-
XX related disorders (thrombosis, atherosclerosis), hyperproliferative
XX disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis),
XX cardiovascular disorders (e.g. arrhythmia), respiratory disorders
XX (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's
XX disease, Parkinson's disease), endocrine disorders (e.g. Addison's
XX disease), reproductive system disorders (e.g. endometriosis), infectious
XX diseases (e.g. viral, bacterial or fungal infections) and
XX gastrointestinal disorders (e.g. Crohn's disease). The invention is also
XX useful to stimulate neuronal growth and treat, prevent, and/or diagnose
XX neuronal damage which occurs in certain neuronal disorders or neuro-
XX degenerative conditions. The present nucleic acid sequence encodes a
XX human DNA-binding protein of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX http.seqdata.uspto.gov/sequence

XX
XX Sequence 222 BP; 112 A; 26 C; 25 G; 57 T; 0 U; 2 Other;

Query Match 0.9%; Score 24; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 145 ATTGACAAAAA 168

RESULT 42
 ABS68209
 ID ABS68209 standard; cDNA; 222 BP.
 AC ABS68209;
 DT 18-NOV-2002 (first entry)
 XX
 DE cDNA encoding human DNA-binding protein #40.
 XX
 KW Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder;
 KW severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease;
 KW diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;
 KW graft-versus-host disease; blood-related disorder; atherosclerosis;
 KW hyperproliferative disorder; cancer; renal disorder; arrhythmia;
 KW acute glomerulonephritis; cardiovascular disorder; respiratory disorder;
 KW Goodpasture's syndrome; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; endocrine disorder; Addison's disease; gene;
 KW reproductive system disorder; endometriosis; infectious disease;
 KW viral infection; bacterial infection; fungal infection; vaccine;
 KW gastrointestinal disorder; multiple sclerosis; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002102638-A1.
 XX
 PD 01-ANG-2002.
 XX
 PF 17-JAN-2001; 2001US-00764846.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216547P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 22-AUG-2000; 2000US-0226868P.
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 PR 01-SEP-2000; 2000US-0229344P.
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 PR 21-SEP-2000; 2000US-0234274P.
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 PR 29-SEP-2000; 2000US-0236327P.
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 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
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 PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
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 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 DR WPI; 2002-690611/74.
 DR P-PSDB; ABG92614.
 XX
 PT Novel DNA-binding protein useful for diagnosis, prognosis, prevention and
 PT treatment of immune, hyperproliferative, respiratory, cardiovascular,
 PT reproductive, endocrine, gastrointestinal and neurological disorders.
 XX
 PS Claim 1; SEQ ID NO 50; 225bp; English.
 XX
 CC The present invention relates to a new DNA-binding protein. The invention
 CC is useful in treating, preventing, diagnosing and/or prognosing
 CC immunodeficiencies (e.g. B cell immunodeficiencies, severe combined
 CC immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple
 CC sclerosis, diabetes mellitus), allergic reactions and conditions (e.g.
 CC asthma), inflammatory conditions, graft-versus-host disease, blood-
 CC related disorders (thrombosis, atherosclerosis), hyperproliferative
 CC disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis),
 CC cardiovascular disorders (e.g. arrhythmia), respiratory disorders
 CC (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease), endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders (e.g. endometriosis), infectious
 CC diseases (e.g. viral, bacterial or fungal infections) and
 CC gastrointestinal disorders (e.g. Crohn's disease). The invention is also
 CC useful to stimulate neuronal growth and treat, prevent, and/or diagnose
 CC neuronal damage which occurs in certain neuronal disorders or neuro-
 CC degenerative conditions. The present nucleic acid sequence encodes a
 CC human DNA-binding protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC http://seqdata.uspto.gov/sequence
 XX
 SQ Sequence 222 BP; 112 A; 26 C; 25 G; 57 T; 0 U; 2 Other;
 XX
 QY Query Match 0.9%; Score 24; DB 6; Length 222;
 QY Best Local Similarity 100.0%; Pred. No. 57;
 Db Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2656 ATTGACAAAAAAAAAAAAAAAAAAAA 2679
 Db 145 ATTGACAAAAAAAAAAAAAAAAAAAA 168
 XX
 RESULT 43
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 ID ADG25203 standard; cDNA; 222 BP.
 AC ADG25203;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human cDNA from extracellular matrix gene 40.
 XX
 KW Extracellular matrix protein; cytosolic; antibacterial; virucide;
 KW neuroprotective; gynaecological; gastrointestinal-gen; candidant;
 KW cardiovascular-gen; nephrotropic; antiinflammatory; muscular-gen;
 KW respiratory-gen; immunosuppressive; cerebroprotective; vasotropic;
 KW neurotropic; antiallergic; cancer; bacterial infection; viral infection;
 KW neural disorder; immune system disorder; blood disorder;

KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW inflammatory disorder; proliferative disorder; human; gene therapy; ss;
gene.
XX Homo sapiens.
XX US2003049650-A1.
XX PD 13-MAR-2003.
XX PD 07-MAR-2002; 2002US-00091483.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764846.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX WPI, 2003-605749/57.
DR P-PSDB; ADC25331.
XX
XX New DNA-binding proteins and gene encoding them, useful for diagnosing,
PT creating and/or preventing e.g. neurological, inflammatory, infectious,
PT cardiovascular, autoimmune, respiratory, neoplastic or digestive
PT diseases.
XX
XX Claim 1; SEQ ID NO 50; 226bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (cDNA)
CC encoding a human extracellular matrix protein, representing one of 161
CC novel genes. Also included are recombinant vectors, host cells
CC (expressing the protein), the extracellular matrix proteins (including
CC their fragments, epitopes and homologues), an isolated antibody that
CC binds specifically to the protein, diagnosing a pathological condition or
CC susceptibility to a pathological condition (comprising determining the
CC presence or absence of a mutation in the nucleic acid and diagnosing a
CC condition based on the presence or absence of the mutation), diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC (comprising determining the presence or amount of expression of the
CC protein in a biological sample and diagnosing a condition based on the
CC presence or amount of expression of the protein), preventing, treating or
CC ameliorating a medical condition by administering the nucleic acid or
CC protein to a mammalian subject, identifying a binding partner to the
CC protein, the gene corresponding to the cDNA sequence, and identifying an
CC activity in a biological assay (comprising expressing the nucleic acid in
CC a cell, isolating the supernatant, detecting an activity in a biological
CC assay and identifying the protein in the supernatant having the
CC activity). The nucleic acids and proteins display the following
CC activities: Cytostatic, antibacterial, Virucide, Neuroprotective,
CC

Query Match 0.9%; Score 24; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2656 ATTGACAAAAA 2679
Db 145 ATTGACAAAAA 168

RESULT 44
ADC25275
ID ADC25275 standard; cDNA; 222 BP.
XX
XX
AC ADC25275;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human cDNA from extracellular matrix gene 112.
XX
XX Extracellular matrix protein; cytotactic; antibacterial; virucide;
XX neuroprotective; gynaecological; gastrointestinal; cardiac;
XX cardiovascular; nephrotoxic; antiinflammatory; muscular; Gen;
XX respiratory; Gen; immunosuppressive; cerebroprotective; vasotrophic;
XX neurotrophic; antiallergic; cancer; bacterial infection; viral infection;
XX neural disorder; immune system disorder; blood disorder;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX inflammatory disorder; proliferative disorder; human; gene therapy; ss;
XX gene.
OS Homo sapiens.
XX

PN US2003049650-A1.
XX
XX 13-MAR-2003
XX
XX 07-MAR-2002; 2002US-00091483.
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XX
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 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Ruben SM, Barash SC;
 XX
 XX WPI; 2003-605749/57.
 DR P-PSDB; ADC25403.
 XX
 PT New DNA-binding proteins and gene encoding them, useful for diagnosing,
 PT treating and/or preventing e.g. neurological, inflammatory, infectious,
 PT cardiovascular, autoimmune, respiratory, neoplastic or digestive
 diseases.
 XX
 PS Claim 1; SEQ ID NO 122; 226bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (cDNA)
 CC encoding a human extracellular matrix protein, representing one of 161
 CC novel genes. Also included are recombinant vectors, host cells
 CC (expressing the protein), the extracellular matrix proteins (including
 CC their fragments, epitopes and homologues), an isolated antibody that
 CC binds specifically to the protein, diagnosing a pathological condition or
 CC susceptibility to a pathological condition (comprising determining the
 CC presence or absence of a mutation in the nucleic acid and diagnosing a
 CC condition based on the presence or absence of the mutation), diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC (comprising determining the presence or amount of expression of the
 CC protein in a biological sample and diagnosing a condition based on the
 CC presence or amount of expression of the protein), preventing, treating or
 CC ameliorating a medical condition by administering the nucleic acid or
 CC protein to a mammalian subject, identifying a binding partner to the
 CC protein, the gene corresponding to the cDNA sequence, and identifying an
 CC activity in a biological assay (comprising expressing the nucleic acid in
 CC a cell, isolating the supernatant, detecting an activity in a biological
 CC assay and identifying the protein in the supernatant having the
 CC activity). The nucleic acids and proteins display the following
 CC activities: Cytostatic, antibacterial, Virolytic, Neuroprotective,
 CC

Query Match 0.9%; Score 24; DB 10; Length 222;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
 DB 145 ATTGACAAAAA 168

RESULT 45
 ABV20036 standard; cDNA; 291 BP.
 XX
 AC ABV20036;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 20027.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX

PI Schlegel R, Endege WO, Monahan JR;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 3266; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 291 BP; 148 A; 32 C; 39 G; 69 T; 0 U; 3 Other;

Query Match 0.9%; Score 24; DB 5; Length 291;
Best Local Similarity 100.0%; Pred.No.55;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAAAAA 2679
|||||
Db 199 ATTGACAAAAAAAAAAAAAAAAAAAA 222

RESULT 46
ABV49795
ID ABV49795 standard; cDNA; 413 BP.
XX
AC ABV49795;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 49786.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JR;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 9711; 11750pp; English.

XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 413 BP; 184 A; 96 C; 49 G; 72 T; 0 U; 12 Other;

Query Match 0.9%; Score 24; DB 5; Length 413;
Best Local Similarity 100.0%; Pred.No.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAAAAA 2679
|||||
Db 224 ATTGACAAAAAAAAAAAAAAAAAAAA 247

RESULT 47
ACH23460
ID ACH23460 standard; cDNA; 474 BP.
XX
AC ACH23460;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult ovary cDNA #1840.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 10672; 44pp; English.

CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
CC
XX
SQ Sequence 474 BP; 169 A; 71 C; 78 G; 154 T; 0 U; 2 Other;

Query Match 0.9%; Score 24; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAA 2679
Db 449 ATTGACAAAAAAAAAAAAAAAAA 472

RESULT 48
ABV60912/c
ID ABV60912 standard; cDNA; 525 BP.
AC ABV60912;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 60903.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI
XX Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 11581; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker

XX
SQ Sequence 525 BP; 112 A; 121 C; 93 G; 199 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 5; Length 525;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAA 2679
Db 35 ATTGACAAAAAAAAAAAAAAAAA 12

RESULT 49
ACC60485
ID ACC60485 standard; cDNA; 532 BP.
XX
AC ACC60485;
XX
DT 23-JUN-2003 (first entry)
XX
DE Rice leaf EST, SEQ ID NO:36.
XX
KW Rice leaf EST; expressed sequence tag; biochip; DNA array; cloning;
KW detection; heterosis; hybrid vigour; transgene detection;
KW herbicide screening; pesticide screening; disease diagnosis;
KW medical research; agriculture; ss.
XX
OS Oryza sativa.
XX
PN CN1364932-A.
XX
PD 21-AUG-2002.
XX
PF 31-OCT-2001; 2001CN-00137662.
XX
PR 31-OCT-2001; 2001CN-00137662.
XX
PA (UYZH-) UNIV ZHEJIANG.
PI
XX Li D, Dong H;
XX
DR WPI; 2003-157852/16.
XX
PT Rice leaf expression sequence labels and constituted biochip.
XX
PS Claim 1; Page 23 (Disclosure); 29pp; Chinese.
XX
CC The invention relates to 50 novel ESTs (expressed sequence tags; ACC60450
CC -ACC60499) obtained from a rice leaf cDNA library. The invention also
CC relates to a biochip comprising these ESTs. The biochip of the invention
CC can be used in a variety of agricultural applications. It can be used in
CC the cloning of genes which confer useful characteristics in crop species,
CC to predict hybrid vigour (heterosis) at an early stage, in the detection
CC of transgenic agricultural produce, in screening for novel herbicides and
CC pesticides and in disease diagnosis. The biochip may also be used in
CC medical research. The present sequence represents a rice leaf EST of the
CC invention
XX
SQ Sequence 532 BP; 140 A; 108 C; 118 G; 166 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 8; Length 532;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAA 2679
Db 507 ATTGACAAAAAAAAAAAAAAAAA 530

RESULT 50
ACF56929
ID ACF56929 standard; cDNA; 532 BP.
XX

AC ACF56929;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Rice leaf EST, SEQ ID NO:36.
 XX
 KM Rice leaf EST; expressed sequence tag; biochip; DNA array; cloning;
 KM detection; heterosis; hybrid vigour; transgene detection;
 KM herbicide screening; pesticide screening; disease diagnosis;
 KM safety assessment; agriculture; plant; ss.
 XX
 OS Oryza sativa.
 XX
 PN CN1366077-A.
 XX
 PD 28-AUG-2002.
 XX
 PF 31-OCT-2001; 2001CN-00137666.
 XX
 PR 31-OCT-2001; 2001CN-00137666.
 XX
 PA (UYZH-) UNTV ZHEJIANG.
 XX
 PI Dong H, L1 D;
 XX
 DR WPI; 2003-382549/37.
 XX
 PT Rice leaf specific expression sequence label and its biochip prepared by
 PT it.
 XX
 PS Claim 1; Page 23 (Disclosure); 0pp; Chinese.
 XX
 CC The invention relates to 50 novel ESTs (expressed sequence tags; ACF5694
 CC -ACF56943) obtained from a rice leaf cDNA library. The invention also
 CC relates to a biochip comprising these ESTs. The biochip of the invention
 CC can be used in a variety of agricultural applications. It can be used in
 CC the cloning of genes which confer useful characteristics in crop species,
 CC to predict hybrid vigour (heterosis) at an early stage, in the detection
 CC of transgenic agricultural produce, in screening for novel herbicides and
 CC pesticides and in disease diagnosis. The biochip may also be used to
 CC assess the safety of transgenic agricultural products. The present
 CC sequence represents a rice leaf EST of the invention
 XX
 SQ Sequence 532 BP; 140 A; 108 C; 118 G; 166 T; 0 U; 0 Other;
 Query Match 0.9%; Score 24; DB 10; Length 532;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAAAAAAAAAAAAAAAAA 2679
 |||||
 DB 507 ATTGACAAAAAAAAAAAAAAAAAAAA 530

Search completed: January 15, 2005, 07:06:48
 Job time : 1324 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 06:17:53 : Search time 8053 Seconds
(without alignments)
12122.444 Million cell updates/sec

Title: US-10-048-046-1

Perfect score: 2679

Sequence: 1 aagaatcgcgcacgagcgccg.....acaaaaaaaaaaaaaaaaaaaaa 2679

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 20

Total number of hits satisfying chosen parameters: 121081

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1497	55.9	2297	3 HSM802304	AL131561 Homo sapi
2	825	30.8	990	1 AL539798	AL539798 AL539798
3	722	27.0	921	5 BUI16559	BUI16559 AGENCOURT
4	703	26.2	992	5 BQ073354	BQ073354 AGENCOURT
5	698	26.1	877	6 CD243458	CD243458 AGENCOURT
6	657	24.5	2412	3 CR625905	CR625905 full-length
7	647	24.2	897	2 BR971929	BR971929 602240332
8	640	23.9	755	7 CN428709	CN428709 170006000
9	620	23.1	840	4 BG395714	BG395714 602458365
10	600	22.4	680	1 AU134937	AU134937 AU134937
11	583	21.8	870	5 BQ215731	BQ215731 AGENCOURT
12	565	21.1	916	4 BM459647	BM459647 AGENCOURT
13	563	21.0	1143	4 BM542545	BM542545 AGENCOURT
14	560	20.9	666	2 BE407732	BE407732 601299777
15	539	20.1	1118	1 AL539797	AL539797 AL539797
16	519	19.4	934	2 BP971838	BP971838 602240424
17	513	19.1	729	6 CA916737	CA916737 3015PRIM2
18	488	18.2	690	2 BE280165	BE280165 601158370
19	479	17.9	694	7 CN428711	CN428711 170006001
20	478	17.8	910	5 BUI18471	BUI18471 AGENCOURT
21	478	17.8	938	5 BQ887242	BQ887242 AGENCOURT
22	477	17.8	1092	4 BM541730	BM541730 AGENCOURT
23	469	17.5	909	5 BX409791	BX409791 BX409791
24	468	17.5	824	1 AU132825	AU132825 AU132825

25	456	17.0	712	2 BE257482	BE257482 60111439
26	456	17.0	1096	4 BG335362	BG335362 602404192
27	452	16.9	1022	4 BM558904	BM558904 AGENCOURT
28	450	16.8	953	5 BQ936072	BQ936072 AGENCOURT
29	447	16.7	938	5 BQ924736	BQ924736 AGENCOURT
30	436	16.3	535	5 BX486289	BX486289 DXF2P686P
31	436	16.3	557	5 BX486564	BX486564 DXF2P686H
32	435	16.2	811	6 CB989147	CB989147 AGENCOURT
33	433	16.2	806	6 CB961597	CB961597 AGENCOURT
34	426	15.9	518	1 AU154212	AU154212 AU154212
35	421	15.7	687	1 AU138310	AU138310 AU138310
36	420	15.7	590	7 CN428707	CN428707 170006002
37	420	15.7	876	5 BQ876252	BQ876252 AGENCOURT
38	418	15.6	650	2 CN428709	CN428709 EST369779
39	414	15.5	414	7 CN428708	CN428708 170005327
40	412	15.4	614	7 CN428710	CN428710 170004553
41	412	15.4	635	4 BG481936	BG481936 602526853
42	409	15.3	490	2 BF109790	BF109790 7169404.x
43	404	15.1	881	5 BUI53737	BUI53737 AGENCOURT
44	394	14.7	940	5 BX409790	BX409790 BX409790
45	386	14.4	475	1 AI200393	AI200393 fE86e04.x
46	386	14.4	618	7 CN481126	CN481126 hw03c10.y
47	382	14.3	824	4 BG831289	BG831289 602766120
48	381	14.2	797	4 BI460002	BI460002 603201532
49	364	13.6	1070	4 BM802324	BM802324 AGENCOURT
50	354	13.2	636	2 BE407797	BE407797 601299183
51	335	12.5	697	4 BG473597	BG473597 602515946
52	326	12.2	527	2 BP439206	BP439206 hab60h05.y
53	323	12.1	647	7 CN428706	CN428706 170006000
54	320	11.9	722	1 AU135780	AU135780 AU135780
55	319	11.9	982	5 BQ943529	BQ943529 AGENCOURT
56	310	11.6	483	1 AA683616	AA683616 fE38fE1.8
57	286	11.0	947	4 BG338730	BG338730 602436491
58	283	10.9	362	2 BF756545	BF756545 QV3-CT055
59	283	10.9	383	1 AV646074	AV646074 AV646074
60	293	10.8	395	1 AV646079	AV646079 AV646079
61	288	10.8	600	2 AM753530	AM753530 PM3-CT026
62	282	10.5	409	5 BX955946	BX955946 DXF2P7810
63	281	10.5	625	2 AM578627	AM578627 PM3-CT026
64	279	10.4	459	1 AA223601	AA223601 zT09a11.x
65	275	10.3	1113	1 AL528042	AL528042 AL528042
66	271	10.1	1050	1 AL561570	AL561570 AL561570
67	262	9.8	333	2 BE858937	BE858937 7640fE03.x
68	247	9.2	337	2 AM589731	AM589731 hg20d07.x
69	245	9.1	352	1 AA281711	AA281711 zT03e12.x
70	244	9.1	690	1 AL046279	AL046279 DXF2P434G
71	241	9.0	724	7 CN428705	CN428705 170005321
72	239	8.9	239	1 AI024825	AI024825 ov35509.x
73	239	8.9	324	1 AA223499	AA223499 zT09b08.8
74	238	8.9	354	1 AA368045	AA368045 EST79479
75	237	8.8	1076	4 BM564304	BM564304 AGENCOURT
76	234	8.7	759	4 BI769973	BI769973 603060267
77	226	8.4	470	1 AA099305	AA099305 zK87e06.x
78	225	8.4	1012	4 BG829969	BG829969 602764383
79	222	8.3	230	1 AA233491	AA233491 zT09a11.8
80	217	8.1	586	4 BI461698	BI461698 603205835
81	210	7.8	614	2 BE937635	BE937635 MRL-TN002
82	204	7.6	364	1 AA281484	AA281484 zT03e12.8
83	198	7.4	635	6 CB269375	CB269375 1008282.H
84	196	7.3	957	1 AL528043	AL528043 AL528043
85	174	6.5	359	4 BG001032	BG001032 RGS-GN013
86	171	6.4	788	7 CR629600	CR629600 DXF2P469H
87	167	6.2	1072	5 BUI181597	BUI181597 AGENCOURT
88	164	6.1	1066	5 BX433224	BX433224 BX433224
89	160	6.0	356	5 BQ354667	BQ354667 RC2-HT097
90	156	5.8	195	2 AM176691	AM176691 RGS-CT008
91	155	5.8	296	1 AA569875	AA569875 tm46h06.8
92	153	5.7	569	2 BE166324	BE166324 QV4-HT049
93	149	5.6	495	5 BX280264	BX280264 BX280264
94	146	5.4	365	2 BF912592	BF912592 RCL-UT008
95	131	4.9	454	2 AM236777	AM236777 xm84h04.x
96	119	4.4	288	1 AA351609	AA351609 EST59398
97	108	4.0	902	5 BX419447	BX419447 BX419447

98	97	406	1	AV747475	AV747475	AV747475	171	37	1.4	406	2	BF137701	BF137701	601782638
99	96	399	7	W96314	W96314	ze10904.r1	172	37	1.4	420	2	BB849327	BB849327	BB849327
100	96	390	7	AL582742	AL582742	AL582742	173	37	1.4	424	5	BY259443	BY259443	BY259443
101	93	350	7	R25085	R25085	Y942F05.r1	174	37	1.4	427	5	BB849818	BB849818	BB849818
102	89	358	4	BG001035	BG001035	RC5-GN013	175	37	1.4	430	5	BY211427	BY211427	BY211427
103	86	231	2	BF912590	BF912590	RC1-UT008	176	37	1.4	438	5	BY218392	BY218392	BY218392
104	86	484	1	AA195342	AA195342	z33307.r	177	37	1.4	501	2	BB866858	BB866858	BB866858
105	84	513	4	BG006974	BG006974	RC2-GN025	178	37	1.4	638	2	BB651462	BB651462	BB651462
106	78	573	5	BX494228	BX494228	DKF2P779A	179	37	1.4	618	2	BB619120	BB619120	BB619120
107	77	589	1	AI887917	AI887917	CK14Q02.x	180	37	1.4	657	6	BY740567	BY740567	BY740567
108	75	109	2	BF905513	BF905513	CM1-MT023	181	37	1.4	657	6	BY740588	BY740588	BY740588
109	75	188	2	BF912591	BF912591	RC1-UT008	182	37	1.4	658	2	BB616065	BB616065	BB616065
110	73	1341	4	EM046514	EM046514	603626565	183	37	1.4	660	2	BB60102	BB60102	BB60102
111	67	518	2	AW798156	AW798156	CM0-UM004	184	37	1.4	662	6	BY737968	BY737968	BY737968
112	67	518	2	BE939377	BE939377	CM0-UM003	185	37	1.4	669	4	BI684350	BI684350	BI684350
113	67	518	4	BF985087	BF985087	CM0-UM003	186	37	1.4	694	6	BY748935	BY748935	BY748935
114	67	522	2	AW798199	AW798199	CM0-UM004	187	37	1.4	702	5	BO179160	BO179160	BO179160
115	67	522	2	BE939388	BE939388	CM0-UM003	188	37	1.4	712	5	BO053419	BO053419	BO053419
116	67	522	4	BF985010	BF985010	CM0-UM003	189	37	1.4	713	6	BY741565	BY741565	BY741565
117	61	991	2	BF979455	BF979455	602288003	190	37	1.4	743	6	BY741076	BY741076	BY741076
118	57	511	4	BI461775	BI461775	603202450	191	37	1.4	779	4	BI158794	BI158794	BI158794
119	54	2.0	1	AI967983	AI967983	W11E07.x	192	37	1.4	781	6	CA327598	CA327598	CA327598
120	53	811	1	BF897610	BF897610	RC1-MT016	193	37	1.4	835	3	AK052473	AK052473	AK052473
121	52	1.9	5	BO003832	BO003832	UI-H-E11	194	37	1.4	975	5	BU513892	BU513892	BU513892
122	50	698	5	BI040246	BI040246	CM4-NT028	195	35	1.3	365	5	BY212187	BY212187	BY212187
123	42	315	4	BI655031	BI655031	WB66C07.x	196	35	1.3	487	7	RS3663	RS3663	RS3663
124	41	375	2	AW197022	AW197022	XM38A12.x	197	34	1.3	407	6	CB771636	CB771636	CB771636
125	42	312	4	BI029077	BI029077	IL5-MT026	198	34	1.3	416	6	BY189062	BY189062	BY189062
126	38	373	4	AI594157	AI594157	VM09A02.Y	199	34	1.3	423	6	CB797276	CB797276	CB797276
127	38	412	1	AA646056	AA646056	VM09A02.Y	200	34	1.3	737	7	CF794729	CF794729	CF794729
128	38	442	2	BF883994	BF883994	PM3-PT020	201	34	1.3	825	7	CK597604	CK597604	CK597604
129	38	445	2	BI270018	BI270018	BY270018	202	33	1.2	262	5	BY259464	BY259464	BY259464
130	38	452	1	AA896707	AA896707	YY09A10.r	203	33	1.2	671	7	CF897125	CF897125	CF897125
131	38	470	7	CF902991	CF902991	A0348F04-	205	33	1.2	276	5	EA457495	EA457495	EA457495
132	38	576	7	CF902991	CF902991	A0245B05-	206	32	1.2	351	4	BO090346	BO090346	BO090346
133	38	677	7	CF898821	CF898821	A0245B05-	207	32	1.2	380	2	BF730034	BF730034	BF730034
134	38	680	7	CF898821	CF898821	UI-M-FB0-	208	32	1.2	429	2	BF601272	BF601272	BF601272
135	38	752	5	BQ749029	BQ749029	UI-M-FB0-	209	32	1.2	432	2	BE847676	BE847676	BE847676
136	38	759	4	BI663013	BI663013	603286404	210	32	1.2	440	5	BY433674	BY433674	BY433674
137	38	787	7	CF410231	CF410231	CH3H065.F	211	32	1.2	448	2	BE848479	BE848479	BE848479
138	38	799	4	AU080847	AU080847	AU080847	212	32	1.2	476	2	BE632090	BE632090	BE632090
139	38	800	4	BI684114	BI684114	603306513	213	32	1.2	476	4	BO074216	BO074216	BO074216
140	38	801	4	BI454758	BI454758	603347118	214	32	1.2	487	4	BE382326	BE382326	BE382326
141	38	902	4	BI695848	BI695848	AGENCOCURT	215	32	1.2	483	2	BE953486	BE953486	BE953486
142	38	940	5	BQ934867	BQ934867	Mus muscu	216	32	1.2	492	1	AA116618	AA116618	AA116618
143	38	3146	3	AK074629	AK074629	Mus muscu	217	32	1.2	502	4	BM106392	BM106392	BM106392
144	38	3146	3	AK074629	AK074629	Mus muscu	218	32	1.2	532	2	BE950094	BE950094	BE950094
145	37	324	5	BY124612	BY124612	BY124612	219	32	1.2	542	2	BE957273	BE957273	BE957273
146	37	324	5	BY784663	BY784663	BY784663	220	32	1.2	545	2	BE946900	BE946900	BE946900
147	37	326	5	BY325437	BY325437	BY325437	221	32	1.2	576	4	EM195052	EM195052	EM195052
148	37	327	5	BY331006	BY331006	BY331006	222	32	1.2	572	4	BM877017	BM877017	BM877017
149	37	328	5	BY191573	BY191573	BY191573	223	32	1.2	576	4	BE853103	BE853103	BE853103
150	37	329	5	BY139817	BY139817	BY139817	224	32	1.2	577	1	AV300531	AV300531	AV300531
151	37	331	5	BY331340	BY331340	BY331340	225	32	1.2	654	2	BB393272	BB393272	BB393272
152	37	334	5	BY328971	BY328971	BY328971	226	32	1.2	665	4	BE695577	BE695577	BE695577
153	37	346	5	BY138514	BY138514	BY138514	227	32	1.2	673	6	BY760885	BY760885	BY760885
154	37	346	5	BY138514	BY138514	BY138514	228	32	1.2	697	7	CM457144	CM457144	CM457144
155	37	354	5	BY104232	BY104232	BY104232	229	32	1.2	717	7	BM945538	BM945538	BM945538
156	37	355	5	BY128116	BY128116	BY128116	230	32	1.2	746	5	BY783931	BY783931	BY783931
157	37	359	5	BY190379	BY190379	BY190379	231	32	1.2	857	6	CB588493	CB588493	CB588493
158	37	359	5	BY202204	BY202204	BY202204	232	32	1.2	864	6	CB320883	CB320883	CB320883
159	37	362	5	BY083949	BY083949	BY083949	233	32	1.2	911	4	BG973906	BG973906	BG973906
160	37	363	5	BY174876	BY174876	BY174876	234	32	1.2	993	6	BY763116	BY763116	BY763116
161	37	365	5	BY065767	BY065767	BY065767	235	31	1.2	341	6	BY783931	BY783931	BY783931
162	37	366	5	BY212180	BY212180	BY212180	236	31	1.2	344	5	BY142662	BY142662	BY142662
163	37	371	5	BY079462	BY079462	BY079462	237	31	1.2	351	5	BY140544	BY140544	BY140544
164	37	375	5	BY065600	BY065600	BY065600	238	31	1.2	362	2	BB770723	BB770723	BB770723
165	37	375	5	BY088272	BY088272	BY088272	239	31	1.2	649	2	BB611775	BB611775	BB611775
166	37	382	5	BY097925	BY097925	BY097925	240	31	1.2	715	7	CF533524	CF533524	CF533524
167	37	384	5	BY264624	BY264624	BY264624	241	30	1.1	429	2	BE234050	BE234050	BE234050
168	37	393	5	BY095790	BY095790	BY095790	242	30	1.1	532	9	CE292415	CE292415	CE292415
169	37	394	5	BY094181	BY094181	BY094181	243	30	1.1	792	4	BI456181	BI456181	BI456181

244	30	1.1	942	4	BI153152	BI153152 602915777	317	26	1.0	259	7	CF902940
245	29	1.1	325	7	H31570	EST105722 R	318	26	1.0	261	9	AJ596535
246	29	1.1	371	5	BY216213	BY216213 BY216213	319	26	1.0	337	6	CD552476
247	29	1.1	408	1	AA914377	AA914377 VY9409.F	320	26	1.0	342	5	BQ337798
248	29	1.1	416	7	CO255478	CO255478 WS00825.B	321	26	1.0	349	6	BY793356
249	29	1.1	435	9	CE499511	CE499511 C1gr-g88	322	26	1.0	354	4	BM164166
250	29	1.1	438	2	AM535019	AM535019 UI-R-BSO-	323	26	1.0	359	2	BF399894
251	29	1.1	440	1	AA068795	AA068795 mm60610.F	324	26	1.0	377	7	CK333598
252	29	1.1	499	6	CD551597	CD551597 BQ330P11-	325	26	1.0	377	7	CK333598
253	29	1.1	510	6	CA530707	CA530707 CO301G07-	326	26	1.0	394	6	CB776715
254	29	1.1	530	4	BG086922	BG086922 H3132C07-	327	26	1.0	414	2	BF562244
255	29	1.1	531	2	BF884751	BF884751 PM3-ET020	328	26	1.0	425	5	BM992402
256	29	1.1	531	6	CB718896	CB718896 AMGNNUC.N	329	26	1.0	431	7	CO213618
257	29	1.1	539	1	AA516857	AA516857 vB88606.F	330	26	1.0	444	6	CA530691
258	29	1.1	541	7	CF897958	CF897958 A0232B12-	331	26	1.0	450	5	CB742272
259	29	1.1	542	6	CA544147	CA544147 CO644D01-	332	26	1.0	467	5	BY007841
260	29	1.1	548	6	CD549550	CD549550 BQ299D05-	333	26	1.0	475	4	BM480991
261	29	1.1	549	2	BB772731	BB772731 BB772731	334	26	1.0	498	7	CF513644
262	29	1.1	556	6	CA579100	CA579100 KO732G08-	335	26	1.0	501	4	BI275343
263	29	1.1	563	6	CD544861	CD544861 BQ261B04-	336	26	1.0	509	7	CF513731
264	29	1.1	565	2	CN670509	CN670509 A0894A05-	337	26	1.0	526	4	BM480930
265	29	1.1	595	7	BE120149	BE120149 UI-R-CAO-	338	26	1.0	539	7	CF373177
266	29	1.1	600	5	BU922139	BU922139 7014-34 M	339	26	1.0	545	2	BE107896
267	29	1.1	606	7	CN700747	CN700747 E0440C08-	340	26	1.0	556	5	CE169926
268	29	1.1	610	7	CN683734	CN683734 E0182G12-	341	26	1.0	556	5	CB982711
269	29	1.1	610	7	CF897650	CF897650 A0227H06-	342	26	1.0	567	6	CB982778
270	29	1.1	662	7	BM950953	BM950953 UI-M-EGO-	343	26	1.0	593	5	BM870883
271	29	1.1	701	5	BM951070	BM951070 UI-M-EGO-	344	26	1.0	614	7	CN688502
272	29	1.1	708	7	CO424828	CO424828 UI-M-HUD-	345	26	1.0	613	9	CE715298
273	29	1.1	727	7	CPA10232	CPA10232 CH3#065.F	346	26	1.0	645	8	AZ566120
274	29	1.1	782	5	BM944161	BM944161 UI-M-EHD-	347	26	1.0	618	5	AX087630
275	29	1.1	817	5	BQ572677	BQ572677 UI-M-FDO-	348	26	1.0	650	5	BM856578
276	29	1.1	824	5	BY025818	BY025818 BY025818	349	26	1.0	650	5	BY129436
277	28	1.0	371	1	AA427279	AA427279 VQ47911.B	350	26	1.0	662	5	BM856077
278	28	1.0	440	1	BY031010	BY031010 BY031010	351	26	1.0	663	1	AV271041
279	28	1.0	442	5	BB853053	BB853053 BB853053	352	26	1.0	675	5	BM861663
280	28	1.0	470	2	AA591859	AA591859 vK91H07.8	353	26	1.0	681	6	CP113998
281	28	1.0	493	2	BB485402	BB485402 BB485402	354	26	1.0	687	5	CR340796
282	28	1.0	656	2	BY760864	BY760864 BY760864	355	26	1.0	696	5	CK837673
283	28	1.0	730	6	CO045302	CO045302 UI-M-HUD-	356	26	1.0	705	5	BM866668
284	28	1.0	747	7	CK780657	CK780657 UI-M-HUD-	357	26	1.0	705	5	BM866668
285	28	1.0	785	7	BU725949	BU725949 SMCLE04	358	26	1.0	711	5	BM867230
286	27	1.0	450	1	AJ686544	AJ686544 AJ686544	359	26	1.0	719	7	CK474059
287	27	1.0	464	3	CR705272	CR705272 Tetraodon	360	26	1.0	733	5	BM875236
288	27	1.0	485	3	CR710885	CR710885 Tetraodon	361	26	1.0	733	5	BM875236
289	27	1.0	529	3	CR706211	CR706211 Tetraodon	362	26	1.0	753	6	CB329950
290	27	1.0	537	3	CR713341	CR713341 Tetraodon	363	26	1.0	767	6	CA327827
291	27	1.0	537	3	CR714569	CR714569 Tetraodon	364	26	1.0	769	5	BU758712
292	27	1.0	537	3	CR716460	CR716460 Tetraodon	365	26	1.0	791	5	BM855996
293	27	1.0	537	3	CR718287	CR718287 Tetraodon	366	26	1.0	800	3	CR706954
294	27	1.0	537	3	CR717649	CR717649 AMGNNUC.U	367	26	1.0	824	3	CR178958
295	27	1.0	554	3	CR706205	CR706205 Tetraodon	368	26	1.0	838	7	CO393246
296	27	1.0	554	3	CR712155	CR712155 Tetraodon	369	26	1.0	858	7	CR434896
297	27	1.0	575	3	BQ186149	BQ186149 UI-E-BJ1-	370	26	1.0	870	4	BC391820
298	27	1.0	612	5	CR713629	CR713629 Tetraodon	371	26	1.0	873	7	CN806455
299	27	1.0	636	3	CR715719	CR715719 Tetraodon	372	26	1.0	901	5	BM700041
300	27	1.0	695	3	CR717775	CR717775 Tetraodon	373	26	1.0	917	2	BF159431
301	27	1.0	750	3	CR707857	CR707857 Tetraodon	374	26	1.0	1318	1	BC018578
302	27	1.0	779	3	CR717351	CR717351 Tetraodon	375	26	1.0	149	6	BI942178
303	27	1.0	782	3	CR708282	CR708282 Tetraodon	376	26	1.0	213	1	AU161609
304	27	1.0	823	3	CR713245	CR713245 Tetraodon	377	26	1.0	249	6	CD572475
305	27	1.0	830	3	CR716505	CR716505 Tetraodon	378	26	1.0	255	2	AI834589
306	27	1.0	830	3	CR717353	CR717353 Tetraodon	379	26	1.0	255	2	AA882705
307	27	1.0	938	3	BI754967	BI754967 603023602	380	26	1.0	276	1	AA882705
308	27	1.0	1024	4	BI754967	BI754967 603023602	381	26	1.0	299	1	AA882705
309	27	1.0	1040	4	BI754967	BI754967 603023602	382	26	1.0	308	2	BF459222
310	27	1.0	126	4	BI845452	BI845452 f896H06.Y	383	26	1.0	317	2	CF902940
311	26	1.0	148	5	BQ255505	BQ255505 NISC_J901	384	26	1.0	337	6	AJ596535
312	26	1.0	161	4	BI881555	BI881555 f87B10.Y	385	26	1.0	342	5	BM870883
313	26	1.0	245	4	BI381109	BI381109 BFLG1_002	386	26	1.0	349	6	BY793356
314	26	1.0	257	4	BI936138	BI936138 PFEStoa2	387	26	1.0	354	4	BM164166
315	26	1.0	257	4	BI936138	BI936138 PFEStoa2	388	26	1.0	359	2	BF399894
316	26	1.0	257	4	BI936138	BI936138 PFEStoa2	389	26	1.0	377	7	CK333598

C 390	25	0.9	320	1	CN845533	EST3184.Z	C 463	25	0.9	733	8	B2512947	B2512947	BOMRR696TR
C 391	25	0.9	323	1	AJ4999321	AJ4999321	C 464	25	0.9	744	5	B0621323	B0621323	UI-H-FLI-
C 392	25	0.9	328	7	CN845576	EST3327.Z	C 465	25	0.9	751	5	BX854501	BX854501	BX854501
C 393	25	0.9	330	4	B6631144	GC-68FLCL	C 466	25	0.9	752	7	COS26125	3530 1.17	COS26125
C 394	25	0.9	336	2	BF459191	UI-M-B21-	C 467	25	0.9	760	5	BQ574633	UI-H-E21-	BQ574633
C 395	25	0.9	338	6	C8348971	C8348971	C 468	25	0.9	767	6	CF202832	CF202832	CF202832
C 396	25	0.9	338	6	C8065090	LIQR-G8-	C 469	25	0.9	806	6	CF210154	CAB20005-	CF210154
C 397	25	0.9	354	6	C8349057	C8349057	C 470	25	0.9	806	6	BI754292	603023110	BI754292
C 398	25	0.9	358	6	CN1944348	C82SG000	C 471	25	0.9	832	4	CO213597	WS00929.B	CO213597
C 399	25	0.9	385	1	AA805395	OB44QD2.8	C 472	25	0.9	900	7	CO774976	ILLUMIGEN	CO774976
C 400	25	0.9	386	2	BF921621	UI-R-AI-e	C 473	25	0.9	1000	7	CN643611	ILLUMIGEN	CN643611
C 401	25	0.9	416	5	BQ449658	IAA442C06.	C 474	25	0.9	51	6	CP420124	rj18e03.Y	CP420124
C 402	25	0.9	438	7	CO239443	WS00725.B	C 475	24	0.9	64	1	AL895948	AL895948	AL895948
C 403	25	0.9	443	2	BF237904	601844480	C 476	24	0.9	101	6	CA901850	PCSC10944	CA901850
C 404	25	0.9	467	5	BM941312	UI-M-B21-	C 477	24	0.9	116	1	AJ250725	q2x3b10.X	AJ250725
C 405	25	0.9	467	5	BM941312	UI-M-B21-	C 478	24	0.9	122	5	BUS65939	AGENCOURT	BUS65939
C 406	25	0.9	502	6	CB330604	SPB5T62b	C 479	24	0.9	136	1	AJ251048	qx71c06.X	AJ251048
C 407	25	0.9	504	6	BM197557	CO301E07-	C 480	24	0.9	142	1	AL663645	AL663645	AL663645
C 408	25	0.9	505	6	CD549519	B029PD05-	C 481	24	0.9	149	6	CF228943	PLAAM019	CF228943
C 409	25	0.9	506	5	BM959031	PLATE 4_F	C 482	24	0.9	152	5	BM952314	IC57Y06.Y	BM952314
C 410	25	0.9	508	2	BM765523	BM765523	C 483	24	0.9	159	4	BM523777	ShEST4a26	BM523777
C 411	25	0.9	510	2	BM753626	BM753626	C 484	24	0.9	163	6	CB340469	CA23E1021	CB340469
C 412	25	0.9	514	4	BM092864	mac19f1f2.	C 485	24	0.9	164	1	AJ308288	tb4z406.X	AJ308288
C 413	25	0.9	521	2	BB852278	uw24c06.X	C 486	24	0.9	164	6	CF202219	CF202219	CF202219
C 414	25	0.9	522	7	CF405492	CSECS054E	C 487	24	0.9	168	6	CP872722	CAB30001	CP872722
C 415	25	0.9	523	6	CD724357	MK_4_13_P	C 488	24	0.9	168	1	AL685139	AL685139	AL685139
C 416	25	0.9	528	2	BM766596	BM766596	C 489	24	0.9	170	6	CA811854	CA811854	CA811854
C 417	25	0.9	530	2	BM766596	BM766596	C 490	24	0.9	172	6	CA811866	CA411N031	CA811866
C 418	25	0.9	531	2	BM023351	dfl10909.Y	C 491	24	0.9	177	1	AJ349237	ca74e02.X	AJ349237
C 419	25	0.9	532	2	AM553385	L0226D12	C 492	24	0.9	177	4	BI306502	NL_4_P04	BI306502
C 420	25	0.9	534	4	BM553385	EST67B03.Y	C 493	24	0.9	179	6	CF202273	CF202273	CF202273
C 421	25	0.9	538	1	AI599732	EST251435	C 494	24	0.9	180	6	CA812341	CA812341	CA812341
C 422	25	0.9	538	4	BM203327	CO252F08-	C 495	24	0.9	183	6	CB340035	CB340035	CB340035
C 423	25	0.9	539	2	AM552599	L0215E03-	C 496	24	0.9	191	7	CN798510	DI4P01902	CN798510
C 424	25	0.9	544	7	CK936679	CGF100451	C 497	24	0.9	199	1	AI254872	qv36c10.X	AI254872
C 425	25	0.9	547	2	BB852833	uw34h10.X	C 498	24	0.9	200	6	CA592486	bsh1_PK00	CA592486
C 426	25	0.9	548	3	CR118744	Tetraddon	C 499	24	0.9	204	1	AA909006	BSBMF520	AA909006
C 427	25	0.9	548	4	BM726890	UI-E-E0-	C 500	24	0.9	208	7	BM032186	497807.MA	BM032186
C 428	25	0.9	548	5	BM932129	UI-E-E01-	C 501	24	0.9	215	2	BE057713	BE057713	BE057713
C 429	25	0.9	548	5	BU741175	UI-R-B81-	C 502	24	0.9	218	7	CO818827	CSECS120C	CO818827
C 430	25	0.9	551	4	BM685132	UI-E-E01-	C 503	24	0.9	232	1	AA721416	n274C01.B	AA721416
C 431	25	0.9	552	5	BM041088	gd33f02.Y	C 504	24	0.9	246	1	AA909550	o18c05.B	AA909550
C 432	25	0.9	554	5	BX564169	BX564169	C 505	24	0.9	250	6	CD272924	T143B0316	CD272924
C 433	25	0.9	557	8	AO955512	LBRAP43TF	C 506	24	0.9	271	4	BM920506	BM920506	BM920506
C 434	25	0.9	558	4	BM677007	h174d01.X	C 507	24	0.9	273	7	CN477670	CN477670	CN477670
C 435	25	0.9	559	5	BQ085477	1h76e08.X	C 508	24	0.9	275	4	BM032186	497807.MA	BM032186
C 436	25	0.9	562	2	BE117469	UI-R-B81-	C 509	24	0.9	280	7	CF380232	CF380232	CF380232
C 437	25	0.9	569	7	CO537250	tah6e02.Y	C 510	24	0.9	280	7	CO049276	EST1533.Z	CO049276
C 438	25	0.9	573	1	AI834391	606067D12	C 511	24	0.9	282	2	BE053047	GA.Ea002	BE053047
C 439	25	0.9	575	1	AJ500651	AJ500651	C 512	24	0.9	284	7	CK385519	lacr72f03.	CK385519
C 440	25	0.9	578	2	BP272747	GA_EB001	C 513	24	0.9	286	7	CF379832	CF379832	CF379832
C 441	25	0.9	588	7	CF946176	wad14c07.	C 514	24	0.9	293	7	CF354806	lacr18e05.	CF354806
C 442	25	0.9	590	7	CK493133	rswab0_01	C 515	24	0.9	294	1	AI619357	486093C01	AI619357
C 443	25	0.9	608	1	AV222940	AV222940	C 516	24	0.9	294	1	AL666206	MCBA05F01	AL666206
C 444	25	0.9	612	9	C8039972	LIQR-G8-	C 517	24	0.9	294	1	CF383497	lacr58b03.	CF383497
C 445	25	0.9	623	1	AJ500168	AJ500168	C 518	24	0.9	296	7	CO251379	WS00813.B	CO251379
C 446	25	0.9	624	5	B0184708	UI-E-E01-	C 519	24	0.9	297	2	BE114409	UI-R-CAO-	BE114409
C 447	25	0.9	627	1	AA701740	PMIRFG_102	C 520	24	0.9	300	5	BUS08884	UI-CF-FNO	BUS08884
C 448	25	0.9	627	1	AJ500531	AJ500531	C 521	24	0.9	301	2	AM102417	sd87f05.Y	AM102417
C 449	25	0.9	629	7	CN103640	EC2CA21C	C 522	24	0.9	301	7	CO221534	WS01015.B	CO221534
C 450	25	0.9	629	7	CO210305	WS00917.B	C 523	24	0.9	305	4	BM360922	A0018-R.	BM360922
C 451	25	0.9	648	7	CE769098	LIQR-G8-	C 524	24	0.9	313	7	CF383657	lacr08d01.	CF383657
C 452	25	0.9	673	7	CN621396	HRO4424.G	C 525	24	0.9	314	7	CO251654	WS00814.B	CO251654
C 453	25	0.9	684	5	CD370760	UI-H-FTL-	C 526	24	0.9	316	4	B6226872	CC-estf1CL	B6226872
C 454	25	0.9	689	3	AIY066742	Schmidtea	C 527	24	0.9	318	7	CR896625	SGP158763	CR896625
C 455	25	0.9	693	6	CF233601	PLAUX002	C 528	24	0.9	321	6	CB258105	B005B09.O	CB258105
C 456	25	0.9	700	6	CB972203	CAB10006-	C 529	24	0.9	325	4	BM080836	sak43d10.	BM080836
C 457	25	0.9	701	8	AO237069	RPC111-71	C 530	24	0.9	329	5	B0739539	PFEStoab4	B0739539
C 458	25	0.9	702	5	BU725338	SIMCDAL1	C 531	24	0.9	335	5	BU496115	PFEStoac0	BU496115
C 459	25	0.9	703	5	BU725374	SIMCD012	C 532	24	0.9	337	7	CO251601	WS00814.B	CO251601
C 460	25	0.9	705	7	CO818832	CSECS120C	C 533	24	0.9	346	6	CB722169	jme607B03	CB722169
C 461	25	0.9	711	6	BQ187519	UI-E-E01-	C 534	24	0.9					
C 462	25	0.9	730	6	CB325928	UI-R-D20-	C 535	24	0.9					

536	24	0.9	348	6	CD273639	CD273639	1143B0282	609	24	0.9	477	1	AV406083
537	24	0.9	348	6	CD274003	CD274003	1143B0381	610	24	0.9	477	5	BU013305
538	24	0.9	348	7	CK895613	CK895613	SGP158132	611	24	0.9	478	7	CN819433
539	24	0.9	349	6	CD273465	CD273465	1143B0473	612	24	0.9	479	7	CN096327
540	24	0.9	349	6	CD275193	CD275193	1143B0172	613	24	0.9	480	2	BE777066
541	24	0.9	350	6	CD272732	CD272732	1143B0487	614	24	0.9	492	1	AU101926
542	24	0.9	351	2	BE881134	BE881134	601492004	615	24	0.9	493	4	BG555269
543	24	0.9	352	6	CD273936	CD273936	1143B0103	616	24	0.9	493	3	CR450127
544	24	0.9	354	6	CD415372	CD415372	GM_CK5478	617	24	0.9	494	2	AM444467
545	24	0.9	356	6	CB722234	CB722234	1143B0907	618	24	0.9	495	4	BM380458
546	24	0.9	357	6	CF229242	CF229242	PeaXMO023	619	24	0.9	495	6	CB529449
547	24	0.9	361	6	CD272851	CD272851	1143B0357	620	24	0.9	497	1	AL374760
548	24	0.9	362	6	CA520929	CA520929	KS1101810	621	24	0.9	498	1	AM395941
549	24	0.9	365	8	CB046630	CB046630	NISC_gf05	622	24	0.9	498	2	AM395941
550	24	0.9	365	8	AQ498987	AQ498987	HS_5154_B	623	24	0.9	504	4	BI154040
551	24	0.9	371	1	AA165052	AA165052	z089g11.8	624	24	0.9	506	7	CK902431
552	24	0.9	376	6	CD809308	CD809308	LCaO5002C	625	24	0.9	507	2	AM187064
553	24	0.9	376	6	CF517091	CF517091	CAP0004_I	626	24	0.9	507	7	CN083312
554	24	0.9	377	5	BU753839	BU753839	UI-1-Bc1D	627	24	0.9	509	3	CR709881
555	24	0.9	377	5	CD272784	CD272784	1143B0252	628	24	0.9	509	3	CR709881
556	24	0.9	378	6	CD273855	CD273855	1143B0507	629	24	0.9	517	5	BM313657
557	24	0.9	379	1	AA827249	AA827249	WS01016.B	630	24	0.9	519	7	BE138870
558	24	0.9	384	7	CO222720	CO222720	OB59C01.8	631	24	0.9	519	7	CF513823
559	24	0.9	386	2	BE138834	BE138834	xw96b11.x	632	24	0.9	519	7	CF514320
560	24	0.9	386	2	CF517184	CF517184	CAP0004_I	633	24	0.9	522	2	BF008417
561	24	0.9	387	5	BQ482638	BQ482638	kes2409.Y	634	24	0.9	523	1	AL370250
562	24	0.9	388	5	BE578937	BE578937	TK04611.Y	635	24	0.9	526	5	BM337015
563	24	0.9	390	5	BQ703811	BQ703811	946106B08	636	24	0.9	527	2	BE034807
564	24	0.9	391	2	AM061812	AM061812	660012D04	637	24	0.9	528	7	CN079087
565	24	0.9	392	5	BQ482639	BQ482639	kes2411.Y	638	24	0.9	528	4	BM358913
566	24	0.9	394	5	BP769495	BP769495	BP769495	639	24	0.9	529	5	BQ408235
567	24	0.9	396	6	CA608319	CA608319	w11_Pk008	640	24	0.9	530	2	BE055651
568	24	0.9	400	7	CO518364	CO518364	3530_1_11	641	24	0.9	530	4	BG447471
569	24	0.9	401	2	BE118783	BE118783	UI-R-CAO-	642	24	0.9	530	7	CR288181
570	24	0.9	406	1	AV713416	AV713416	AV713416	643	24	0.9	531	3	CR103775
571	24	0.9	406	6	CAY03901	CAY03901	wk1c_Pk0	644	24	0.9	531	4	BG454040
572	24	0.9	408	5	AL380320	AL380320	MCBB51G02	645	24	0.9	532	4	BI813398
573	24	0.9	409	5	BP765181	BP765181	BP765181	646	24	0.9	535	3	CR706693
574	24	0.9	410	2	BF279018	BF279018	GA_EB003	647	24	0.9	535	7	CN045296
575	24	0.9	414	2	BB814407	BB814407	BB814407	648	24	0.9	537	7	CO233632
576	24	0.9	414	4	BI818827	BI818827	BFLG2_000	649	24	0.9	538	7	CK308175
577	24	0.9	417	2	BE511490	BE511490	946061B12	650	24	0.9	539	7	CF513326
578	24	0.9	418	4	BI651749	BI651749	603298535	651	24	0.9	542	7	CF513909
579	24	0.9	420	2	AM519848	AM519848	660054A07	652	24	0.9	542	5	BY476343
580	24	0.9	420	4	BG797366	BG797366	1C14612.X	653	24	0.9	543	7	CF516059
581	24	0.9	420	5	BE978875	BE978875	BX900319	654	24	0.9	544	2	BI770568
582	24	0.9	423	2	BE978875	BE978875	BX900319	655	24	0.9	546	1	AI943061
583	24	0.9	424	1	AL382501	AL382501	MCBC07D07	656	24	0.9	546	4	BM361791
584	24	0.9	429	6	CH761481	CH761481	AMGNNUC.S	657	24	0.9	548	4	BC229825
585	24	0.9	430	2	BE238707	BE238707	946007C04	658	24	0.9	549	2	AM792382
586	24	0.9	430	5	BY375896	BY375896	zmiw8486	659	24	0.9	551	7	CF220651
587	24	0.9	430	7	CK370296	CK370296	747165	660	24	0.9	551	7	CF354374
588	24	0.9	430	7	T47165	T47165	ybs3b06_11	661	24	0.9	552	7	CO207052
589	24	0.9	432	7	CN996278	CN996278	MdFw0441	662	24	0.9	552	7	CO210642
590	24	0.9	435	7	CO221523	CO221523	WS01013.B	663	24	0.9	553	8	BM4227058
591	24	0.9	438	7	CK895238	CK895238	SGP154493	664	24	0.9	556	7	CF516136
592	24	0.9	440	7	CN528487	CN528487	UI-M-HO-	665	24	0.9	557	4	BM520159
593	24	0.9	443	1	AI884251	AI884251	fc76b05.x	666	24	0.9	557	7	CK310041
594	24	0.9	449	1	AI498855	AI498855	AL498855	667	24	0.9	561	6	CA823293
595	24	0.9	452	5	BP769172	BP769172	BP769172	668	24	0.9	565	5	CE187250
596	24	0.9	453	5	BK502704	BK502704	DKF29775J	669	24	0.9	566	5	BP768751
597	24	0.9	457	1	AI629790	AI629790	486039B04	670	24	0.9	567	5	CR897096
598	24	0.9	457	4	BI674794	BI674794	949067D03	671	24	0.9	567	8	AZ960824
599	24	0.9	458	7	CN080112	CN080112	EC2BBA17C	672	24	0.9	570	2	AM792260
600	24	0.9	459	6	CB247587	CB247587	UI-M-FIO-	673	24	0.9	574	1	AL510239
601	24	0.9	460	7	CN084195	CN084195	EC2BBA23D	674	24	0.9	576	4	BI950373
602	24	0.9	460	7	CN086413	CN086413	EC2BBA27A	675	24	0.9	576	4	CA401839
603	24	0.9	460	7	CN106707	CN106707	EC2CA2A28	676	24	0.9	576	6	CB057169
604	24	0.9	461	7	CN083590	CN083590	EC2BBA22D	677	24	0.9	577	6	CE728975
605	24	0.9	462	7	CN078108	CN078108	EC2BBA14B	678	24	0.9	577	1	AJ801354
606	24	0.9	468	7	CO234947	CO234947	WS0263.B2	679	24	0.9	579	7	CN038742
607	24	0.9	475	1	AL385764	AL385764	MCBC30E05	680	24	0.9	579	7	CO253411
608	24	0.9	476	6	CF281803	CF281803	14EFTL--09	681	24	0.9	579	7	AV406083
													BU013305
													CN819433
													CN096327
													BE777066
													AU101926
													BG555269
													CF450127
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													AL374760
													AM395941
													BI154040
													CK902431
													AM187064
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													CR709881
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													CF513823
													CF514320
													BF008417
													AL370250
													BM337015
													BE034807
													CN079087
													BM358913
													BQ408235
													BE055651
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													BI813398
													CR706693
													CN045296
													CO233632
													CK308175
													CF513326
													CF513909
													BY476343

682	24	0.9	579	9	CG988064	CH240.140	C 755	24	0.9	693	7	CO224007	CO224007
683	24	0.9	581	8	AZ308475	IM001IB05	C 756	24	0.9	699	5	BU742309	BU742309
684	24	0.9	582	6	BP747329	BP747329	C 757	24	0.9	707	2	BB246045	BB246045
685	24	0.9	582	6	CA823126	CA823126	C 758	24	0.9	708	7	CO208412	CO208412
686	24	0.9	584	4	BM520022	sak6f10.	C 759	24	0.9	709	4	BG612002	BG612002
687	24	0.9	588	5	BK686655	BK686655	C 760	24	0.9	709	8	BH478600	BH478600
688	24	0.9	588	5	BK878340	BK878340	C 761	24	0.9	710	5	BO603929	BO603929
689	24	0.9	590	7	CF512118	CF512118	C 762	24	0.9	710	7	CO203808	CO203808
690	24	0.9	590	7	CFN079155	CFN079155	C 763	24	0.9	715	2	BF163311	BF163311
691	24	0.9	592	5	BP761317	BP761317	C 764	24	0.9	715	8	BH450224	BH450224
692	24	0.9	593	5	BO542910	BO542910	C 765	24	0.9	716	7	CR280603	CR280603
693	24	0.9	594	7	CO257990	CO257990	C 766	24	0.9	723	4	BM680113	BM680113
694	24	0.9	595	7	BP768688	BP768688	C 767	24	0.9	728	6	CA750810	CA750810
695	24	0.9	601	2	AW761403	AW761403	C 768	24	0.9	732	6	CF211492	CF211492
696	24	0.9	605	7	BQ234367	BQ234367	C 769	24	0.9	740	5	BQ199693	BQ199693
697	24	0.9	608	5	BK369645	BK369645	C 770	24	0.9	742	7	CR933645	CR933645
698	24	0.9	609	1	AI725249	AI725249	C 771	24	0.9	759	2	BE616510	BE616510
699	24	0.9	609	7	CO236410	CO236410	C 772	24	0.9	769	8	BZ492921	BZ492921
700	24	0.9	610	5	BU350549	BU350549	C 773	24	0.9	770	6	CF206006	CF206006
701	24	0.9	610	6	CF322331	CF322331	C 774	24	0.9	777	5	BR623458	BR623458
702	24	0.9	611	2	AM557839	AM557839	C 775	24	0.9	780	7	CR280432	CR280432
703	24	0.9	611	2	CO212309	CO212309	C 776	24	0.9	781	7	CF214902	CF214902
704	24	0.9	612	5	BP775349	BP775349	C 777	24	0.9	786	6	BK748163	BK748163
705	24	0.9	614	5	BO205916	BO205916	C 778	24	0.9	791	5	CK698140	CK698140
706	24	0.9	619	2	AM125941	AM125941	C 779	24	0.9	793	7	CF215147	CF215147
707	24	0.9	621	7	CO238318	CO238318	C 780	24	0.9	796	6	CA505075	CA505075
708	24	0.9	623	5	BQ386943	BQ386943	C 781	24	0.9	797	6	CR507171	CR507171
709	24	0.9	623	7	CF415577	CF415577	C 782	24	0.9	802	3	CR171712	CR171712
710	24	0.9	625	5	BO415211	BO415211	C 783	24	0.9	802	3	CR677705	CR677705
711	24	0.9	625	9	CE101918	CE101918	C 784	24	0.9	804	3	CO396698	CO396698
712	24	0.9	628	5	BO414555	BO414555	C 785	24	0.9	806	7	CR561751	CR561751
713	24	0.9	628	6	CE204031	CE204031	C 786	24	0.9	818	7	CF208969	CF208969
714	24	0.9	629	9	CE363491	CE363491	C 787	24	0.9	821	6	CF201904	CF201904
715	24	0.9	632	6	CA431440	CA431440	C 788	24	0.9	828	5	BK752205	BK752205
716	24	0.9	632	2	BF703601	BF703601	C 789	24	0.9	837	7	CR284330	CR284330
717	24	0.9	633	2	BO091858	BO091858	C 790	24	0.9	837	9	CR113923	CR113923
718	24	0.9	634	7	CF516348	CF516348	C 791	24	0.9	839	1	AV755889	AV755889
719	24	0.9	635	7	BF685191	BF685191	C 792	24	0.9	844	7	CF0726296	CF0726296
720	24	0.9	637	2	CO223366	CO223366	C 793	24	0.9	847	6	CF209163	CF209163
721	24	0.9	639	7	CF512806	CF512806	C 794	24	0.9	857	7	CO213908	CO213908
722	24	0.9	641	1	AI855200	AI855200	C 795	24	0.9	858	2	BE641387	BE641387
723	24	0.9	641	6	CB429183	CB429183	C 796	24	0.9	858	2	CO212102	CO212102
724	24	0.9	641	6	CF312741	CF312741	C 797	24	0.9	859	7	BR677864	BR677864
725	24	0.9	642	6	CN171128	CN171128	C 798	24	0.9	862	2	CK205033	CK205033
726	24	0.9	642	7	CR699328	CR699328	C 799	24	0.9	874	7	BF269927	BF269927
727	24	0.9	643	3	CO203327	CO203327	C 800	24	0.9	881	2	CR676238	CR676238
728	24	0.9	645	7	BM683440	BM683440	C 801	24	0.9	887	4	BM358178	BM358178
729	24	0.9	650	4	CO541533	CO541533	C 802	24	0.9	893	4	CR437127	CR437127
730	24	0.9	655	7	CR054059	CR054059	C 803	24	0.9	895	7	CO765774	CO765774
731	24	0.9	660	9	BQ408628	BQ408628	C 804	24	0.9	907	7	BU161230	BU161230
732	24	0.9	662	5	BK505605	BK505605	C 805	24	0.9	908	5	BK763889	BK763889
733	24	0.9	663	6	CA088398	CA088398	C 806	24	0.9	910	5	CR204684	CR204684
734	24	0.9	663	6	BM990769	BM990769	C 807	24	0.9	923	7	AY067506	AY067506
735	24	0.9	665	5	BU100480	BU100480	C 808	24	0.9	924	3	BI833513	BI833513
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740	24	0.9	676	1	AV726545	AV726545	C 813	24	0.9	1002	2	CC190371	CC190371
741	24	0.9	678	6	CF519231	CF519231	C 814	24	0.9	1013	3	CG190646	CG190646
742	24	0.9	679	7	CK303055	CK303055	C 815	24	0.9	1025	8	CC190646	CC190646
743	24	0.9	680	7	CO219259	CO219259	C 816	24	0.9	1054	4	CC190646	CC190646
744	24	0.9	682	7	CE340709	CE340709	C 817	24	0.9	1076	8	BC001300	BC001300
745	24	0.9	683	7	BO574159	BO574159	C 818	24	0.9	1101	7	CRK08019	CRK08019
746	24	0.9	684	2	BF639790	BF639790	C 819	24	0.9	1147	3	AK042639	AK042639
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749	24	0.9	692	6	CR327782	CR327782	C 822	24	0.9	1233	3	CR686187	CR686187
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C 843	23	0.9	123	7	CO517195	CO517195	B13dSG33G	916	23	0.9	161	1	A1313053	A1313053	qx82c05.x
C 844	23	0.9	127	6	CD747955	CD747955	rw30c01.y	917	23	0.9	161	1	A1305933	A1305933	qx79b03.x
C 845	23	0.9	129	2	AM423388	AM423388	bh65b03.y	918	23	0.9	162	1	A1305933	A1305933	qx79b03.x
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ALIGNMENTS

RESULT 1
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 DEFINITION Homo sapiens mRNA; cDNA DKFp434N2420 (from clone DKFp434N2420).
 ACCESSION AL137561
 VERSION AL137561.1 GI:6808265
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2297)
 Oesterwaelder,B., Obermaier,B., Deutschenbauer,S., Schaipp,A.,
 Mewes,H.W., Weill,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
 Wiemann,S.
 The German cDNA Consortium
 Direct Submission
 Submitted (03-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuberg, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
 sequenced by Medigenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project.
 This clone (DKFp434N2420) is available at the RZPD Deutsches
 Ressourcezentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFp434N2420
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES

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ORIGIN

Query Match 55.9%; Score 1497; DB 3; Length 2297;
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 QY 2005 CGTAATGCGGCACTAGGTTGAAGCTCAACGCAATGAAATTAATCAATCTGCTGA 2064
 DB 841 CGTAATGCGGCACTAGGTTGAAGCTCAACGCAATGAAATTAATCAATCTGCTGA 900
 QY 2065 CAGACAGGTTCAAAAATTAAGCATCAAGAGCCCTGAGAGCTTCAAGCATGAGGTG 2124
 DB 901 CAGACAGGTTCAAAAATTAAGCATCAAGAGCCCTGAGAGCTTCAAGCATGAGGTG 960
 QY 2125 AAGAGAGCGTGTGTTTAAATACAGACAGACAGCTCAAGTGTGTTCAAGCCCTG 2184
 DB 961 AAGAGAGCGTGTGTTTAAATACAGACAGACAGCTCAAGTGTGTTCAAGCCCTG 1020
 QY 2185 AAGGAGAGGACCGAGGCTCTCCGACAGGCTCTGAGGCTGAGCTTCTGAGAGCTTTT 2244
 DB 1021 AAGGAGAGGACCGAGGCTCTCCGACAGGCTCTGAGGCTGAGCTTCTGAGAGCTTTT 1080
 QY 2245 ACCCTCTGAGTGAACCTCCGAGAGCCCGGAGCCGCGCCCTCTGAGAG 2304
 DB 1081 ACCCTCTGAGTGAACCTCCGAGAGCCCGGAGCCCGCGCCCTCTGAGAG 1140
 QY 2305 GCTGGGACAGGCTCTGAGTGAACAGACAGACAGAGCTTCTGATGATGCGG 2364
 DB 1141 GCTGGGACAGGCTCTGAGTGAACAGACAGACAGAGCTTCTGATGATGCGG 1200
 QY 2365 CGTCCCGGACAGGCTCTGAGTGAACAGAGCTTCTGATGATGAGTAAAG 2424
 DB 1201 CGTCCCGGACAGGCTCTGAGTGAACAGAGCTTCTGATGATGAGTAAAG 1260
 QY 2425 AGAAGCTGTTTCAAGAAAGTTCAAGGAGAGAGGCAAGTTTCAAAAATGTT 2484
 DB 1261 AGAAGCTGTTTCAAGAAAGTTCAAGGAGAGAGGCAAGTTTCAAAAATGTT 1320
 QY 2485 TCAGAGAGAGGAGCATTAAGTTTACAGCTCAAGAGCTCAACATATCTGCTGAG 2544
 DB 1321 TCAGAGAGAGGAGCATTAAGTTTACAGCTCAAGAGCTCAACATATCTGCTGAG 1380
 QY 2545 AAAACACAGCATTTTATCTATTTTATTTATTAAGTTGCTTATCTTAAATA 2604
 DB 1381 AAAACACAGCATTTTATCTATTTTATTTATTAAGTTGCTTATCTTAAATA 1440
 QY 2605 GATTTAATGTCACAACTGAGCACAATTAATTAATTAATTAATTAATGAC 2661
 DB 1441 GATTTAATGTCACAACTGAGCACAATTAATTAATTAATTAATTAATGAC 1497

RESULT 2
 AL539798 990 bp mRNA linear EST 24-MAR-2004
 LOCUS AL539798 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF031YA23 5-PRIME, mRNA sequence.
 ACCESSION AL539798
 VERSION AL539798.3 GI:45715436
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 990)
 L1, W.B., Gruber, C., Jessee, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31264361.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequenage
 BP 191 91006 Evry cedex - France
 Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6792.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DF031YA120P1ac=6792.r.
 FEATURES
 Location/Qualifiers
 1..990
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo (dr) primer. Five prime end
 enriched, double-strand cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 30.8%; Score 825; DB 1; Length 990;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 GTTCGGGCGGGGCGGAGTGAATCCGATGAGCGGCCGAGAGGCAAGCAGTGG 120
 DB 20 GTTCGGGCGGGGCGGAGTGAATCCGATGAGCGGCCGAGAGGCAAGCAGTGG 79
 QY 121 CCGCGCGGACGCTCTGAGGAGCGCTCTGAGGCGGAGAGGCGAGCCGAC 180
 DB 80 CCGCGCGGACGCTCTGAGGAGCGCTCTGAGGCGGAGAGGCGAGCCGAC 139
 QY 181 GTTCCTCTGAGGAGGCGGAGTGAATCCGATGAGCGGCCGAGAGGCGAGCTTCTTC 240
 DB 140 GTTCCTCTGAGGAGGCGGAGTGAATCCGATGAGCGGCCGAGAGGCGAGCTTCTTC 199
 QY 241 CCAGCAATTAATCTGCTCTGAGGAGTCACTGATGAATGATGATGAATTAATCAGGT 300
 DB 200 CCAGCAATTAATCTGCTCTGAGGAGTCACTGATGAATGATGATGAATTAATCAGGT 259
 QY 301 CAGGTGACACTGGAAGATACAGACAGAGTGAACAGTATTAACAGCTGAAGTTGT 360
 DB 260 CAGGTGACACTGGAAGATACAGACAGAGTGAACAGTATTAACAGCTGAAGTTGT 319
 QY 361 AAGAGCAGACATGCCCTTTACAGACTGGGAGTGCATCTTGTGTTACAGAAAT 420
 DB 320 AAGAGCAGACATGCCCTTTACAGACTGGGAGTGCATCTTGTGTTACAGAAAT 379
 QY 421 GAACGGAGACAGAGTGCATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 480
 DB 380 GAACGGAGACAGAGTGCATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 439
 QY 481 CAGAGATCTTTGAAGTCAAGAGAAATGTTTCATGAGGACCAAGATACCTCAGGT 540
 DB 440 CAGAGATCTTTGAAGTCAAGAGAAATGTTTCATGAGGACCAAGATACCTCAGGT 499
 QY 541 GCAAGTGCAGGCGGAGGCGGATCCCGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 500 GCAAGTGCAGGCGGAGGCGGATCCCGGATCCCGGATCCCTGCTGCTGCTGCTGCTGCTG 559
 QY 601 TGCCTTGAAGAGACAGAGCATCAACATGAGAGCTGAGAGCTTCCCAACAGCTCGGCG 660
 DB 560 TGCCTTGAAGAGACAGAGCATCAACATGAGAGCTGAGAGCTTCCCAACAGCTCGGCG 619
 QY 661 TCTTCAAGAGAGCTTCTCTGAGGCGAGAGCTTCTCAAGTGTGAGGTCTGAGGAGT 720
 DB 620 TCTTCAAGAGAGCTTCTCTGAGGCGAGAGCTTCTCAAGTGTGAGGTCTGAGGAGT 679
 QY 721 GGTGAGTCTCCCTTAAGAGAGTGTCTCTGAGGCGAGAGTGAATCTTCAAGCTTT 780
 DB 680 GGTGAGTCTCCCTTAAGAGAGTGTCTCTGAGGCGAGAGTGAATCTTCAAGCTTT 739

ORIGIN

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using Zap-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

Query Match 26.2%; Score 703; DB 5; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

551 GGGAGAGGGGGGCGATCCCGGGGTCCTCCGCGTCCGCGCCGACCTCAGTGTGCTTTGAGG 610
1 GGGAGAGGGGGGCGATCCCGGGGTCCTCCGCGTCCGCGCCGACCTCAGTGTGCTTTGAGG 60
611 AACACAGGCCATCAATCGACGTGACACTCTTTCCCAAGCCTCGGCTCTTTCCACGG 670
61 AACACAGGCCATCAATCGACGTGACACTCTTTCCCAAGCCTCGGCTCTTTCCACGG 120
671 AGCTTCTCTCTGACGGGCGGAGACCTTCTCCAGTTGTGGGTCTGGGGGTGTGGCATCT 730
121 AGCTTCTCTCTGACGGGCGGAGACCTTCTCCAGTTGTGGGTCTGGGGGTGTGGCATCT 180
731 CCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGAAGTTCAGCTTGGCTCAGCTC 790
181 CCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGAAGTTCAGCTTGGCTCAGCTC 240
791 TCCACAGACAGAAAGTGTGCTCTTTTCGTCTGTGGAACCCAGATCAGAGAGATTTGG 850
241 TCCACAGACAGAAAGTGTGCTCTTTTCGTCTGTGGAACCCAGATCAGAGAGATTTGG 300
851 AGCCCTGTGAAGAAAGAAATGAGAGAGATGGGACCTTGAACCTTGAACGGGCACTTTGG 910
301 AGCCCTGTGAAGAAAGAAATGAGAGAGATGGGACCTTGAACCTTGAACGGGCACTTTGG 360
911 TGCACACACCGCGTGAAGATGCCCAACCGTCCACGAGAGACGTCAGAGAGCGGCTGGG 970
361 TGCACACACCGCGTGAAGATGCCCAACCGTCCACGAGAGACGTCAGAGAGCGGCTGGG 420
971 AGCCAGACAGATGAGAGAGACGCTGACATGATCATCTGTCAGAGACCTGCTGACAGACT 1030
421 AGCCAGACAGATGAGAGAGACGCTGACATGATCATCTGTCAGAGACCTGCTGACAGACT 480
1031 GCGTGAAGTTTGACGCCCTGATGACACGTTTGGCGGCTTCTACTCGGCTGGATGG 1090
481 GCGTGAAGTTTGACGCCCTGATGACACGTTTGGCGGCTTCTACTCGGCTGGATGG 540
1091 AGGCGTCCGTCGTCCTGCTACCTGCGCGTCCGCGGAGCGGATCTGTAAACACCA 1150
541 AGGCGTCCGTCGTCCTGCTACCTGCGCGTCCGCGGAGCGGATCTGTAAACACCA 600
1151 TCTCTCAACAACCTCGTGAAGATACCTCATCCAGATCCAGACAGAGTCCGAGTGAAG 1210
601 TCTCTCAACAACCTCGTGAAGATACCTCATCCAGATCCAGACAGAGTCCGAGTGAAG 660
1211 AAGATGTGCAAGATGATGATCCAGAGATTAATCACTCAAGA 1253
661 AAGATGTGCAAGATGATGATCCAGAGATTAATCACTCAAGA 703

RESULT 5

LOCUS

CD243458 877 bp mRNA linear EST 22-MAY-2003

DEFINITION AGENCOURT 14121909 NIH_MGC_180 Homo sapiens cDNA clone

IMAGE:30383176 5', mRNA sequence.

ACCESSION

CD243458

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo..

REFERENCE 1 (bases 1 to 877)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: NDM446 row: j column: 17
High quality sequence stop: 660.

FEATURES

source

1..877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30383176"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_1ib="NIH_MGC_180"
/note="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 26.1%; Score 698; DB 6; Length 877;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1527 AGAAGACACGCGCTGTGACCTGTGCTTCCAGCCATGCCGACCGGAGACGGAGCG 1586
4 AGAAGACACGCGCTGTGACCTGTGCTTCCAGCCATGCCGACCGGAGACGGAGCG 63
1587 CGAGCAGACCGCGGTGTGCGCCCTTACAGAGTGTGGGTCTGCTGACGCTTTTGCCA 1646
64 CGAGCAGACCGCGGTGTGCGCCCTTACAGAGTGTGGGTCTGCTGACGCTTTTGCCA 123
1647 CCTGTACTGGGGCTGACCGCGGACCGGCTGTACGCGCTGCGCCGCTTTTGAGCT 1706
124 CCTGTACTGGGGCTGACCGCGGACCGGCTGTACGCGCTGCGCCGCTTTTGAGCT 183
1707 CAACCTGGGTGACAAAGTGTCTGACGCGGTGCTGAACAACAACAGCTACAGTCAAGAT 1766
184 CAACCTGGGTGACAAAGTGTCTGACGCGGTGCTGAACAACAACAGCTACAGTCAAGAT 243
1767 CCTGAAGATTAATCTGGCAACCAAGAGTTTGAATGAGAAAAATGTTGACCGAGAGCT 1826
244 CCTGAAGATTAATCTGGCAACCAAGAGTTTGAATGAGAAAAATGTTGACCGAGAGCT 303
1827 CGTGGCTTCCAGCGGGAGGTGTTTGTGCTGATTAACAAGTCAAGGAGACACCT 1886
304 CGTGGCTTCCAGCGGGAGGTGTTTGTGCTGATTAACAAGTCAAGGAGACACCT 363
1887 TCTGTATTACTCTGTGGGCTGCGAGCTTCCGTGAGTCACTTAAGTATCGGAGAA 1946
364 TCTGTATTACTCTGTGGGCTGCGAGCTTCCGTGAGTCACTTAAGTATCGGAGAA 423
1947 CATTCCTGCTTCCAGAGTTCAGAGTGGCGGTAAATCCGCTCTGACTGAGGCGCG 2006
424 CATTCCTGCTTCCAGAGTTCAGAGTGGCGGTAAATCCGCTCTGACTGAGGCGCG 483
2007 TAACTGCCGCACTCAGTGAAGCTCAACAGCCATGAATTAATCATATCTTGGAACA 2066
484 TAACTGCCGCACTCAGTGAAGCTCAACAGCCATGAATTAATCATATCTTGGAACA 543
2067 GACAAGTTCAAAAATAAGATCAAGAGAGCCCTGAGAGCTTTGAGCACTGAGAGTGA 2126

Db 544 GACAAAGTTCAAAAATAAGATCCAGAGAGCCCTGAGAGCTTTTCAAGCATGAGAGTGA 603

QY 2127 GAGAGGCTTTTAAATATACAGACAGACAGTCAAGGTTTTCACAGCCCTGAG 2186

Db 604 GAGAGGCTTTTAAATATACAGACAGACAGTCAAGGTTTTCACAGCCCTGAG 663

QY 2187 GGAAGGAGCAGAGGCTCTCCGACAGGCTCTGGGGTGAAGCTTTCTGAGAGCTTTTAC 2246

Db 664 GGAAGGAGCAGAGGCTCTCCGACAGGCTCTGGGGTGAAGCTTTCTGAGAGCTTTTAC 723

QY 2247 CCTCTGAGTGAACCTCCCGAGAGCC 2275

Db 724 CCTCTGAGTGAACCTCCCGAGAGCC 752

RESULT 6
CR625905 2412 bp mRNA linear HTC 21-JUL-2004
LOCUS Full-length cDNA clone CS0DF01Y119 of Fetal brain of Homo sapiens (human).
DEFINITION
ACCESSION CR625905 GI:50506712
VERSION HTC, CINSIT, cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
REFERENCE
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 2412)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
COMMENT Location/Qualifiers
FEATURES
source 1..2412
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF01Y119"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 24.5%; Score 657; DB 3; Length 2412;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1772 AGAATTAACCTGACACAGAGTTTGAATGAAACATGTTGACCGAGAGGCTGCTG 1831

Db 950 AGAATTAACCTGACACAGAGTTTGAATGAAACATGTTGACCGAGAGGCTGCTG 1009

QY 1832 CTCTCAGCGGGAGAGTCTCTGCTGTGATTACAGAGTCACGGGAGACACCGTTCTGT 1891

Db 1010 CTCTCAGCGGGAGAGTCTCTGCTGTGATTACAGAGTCACGGGAGACACCGTTCTGT 1069

QY 1892 GTTACTGCTGTGGCTGCGGAGCTTCCGTGAGCTGACCTATCGATTCGGCAGAAATTC 1951

Db 1070 GTTACTGCTGTGGCTGCGGAGCTTCCGTGAGCTGACCTATCGATTCGGCAGAAATTC 1129

QY 1952 CTGCTTCCGAGTTGCAAGTGGCGGTAAATCCGCTGACTGCTGAGGCGGTAAC 2011

Db 1130 CTGCTTCCGAGTTGCAAGTGGCGGTAAATCCGCTGACTGCTGAGGCGGTAACT 1189

QY 2012 GCCGCACTCAGGTGAAAGCTCACCACGCGCATGAAATTCATATCTGTGAACAGACAA 2071

Db 1190 GCCGCACTCAGGTGAAAGCTCACCACGCGCATGAAATTCATATCTGTGAACAGACAA 1249

QY 2072 GTTTCAAAATACTAAGCATCCGAGAGGCTTGAAGAGCTTTTCAAGAGCTGAGAGAG 2131

Db 1250 GTTTCAAAATACTAAGCATCCGAGAGGCTTGAAGAGCTTTTCAAGAGCTGAGAGAG 1309

QY 2132 CGTGTGTTTAAATATACAGACAGACAGTCAAGGTTTTCACAGCCCTGAGGGAAG 2191

Db 1310 CGTGTGTTTAAATATACAGACAGACAGTCAAGGTTTTCACAGCCCTGAGGGAAG 1369

QY 2192 GAGCGAGGCTCTCCGACAGGCTCTGGGGTGAAGCTTTCTGTGAGAGCTTTTACCTCT 2251

Db 1370 GAGCGAGGCTCTCCGACAGGCTCTGGGGTGAAGCTTTCTGTGAGAGCTTTTACCTCT 1427

QY 2252 GAGTGAAGCTCTCCGAGAGGCTCTGGGGTGAAGCTTTCTGTGAGAGCTTTTACCTCT 2311

Db 1428 GAGTGAAGCTCTCCGAGAGGCTCTGGGGTGAAGCTTTCTGTGAGAGCTTTTACCTCT 1487

QY 2312 AGGCTCTGCTGTCATCAGACAGACAGACAGCTTTCTGTATCATGTCGCGCTCCG 2371

Db 1488 AGGCTCTGCTGTCATCAGACAGACAGACAGCTTTCTGTATCATGTCGCGCTCCG 1547

QY 2372 CCGAGAGGCGAGGTTTGGCTCTTTTGTATCATTTTCCGAACTACAGTTAAAGCAGAGTC 2431

Db 1548 CCGAGAGGCGAGGTTTGGCTCTTTTGTATCATTTTCCGAACTACAGTTAAAGCAGAGTC 1607

QY 2432 TGTGTTTCAAGAAAGTTTCAAGGAGAGGCGCAAGTTATCAAAAACATGTTTCAGAG 2491

Db 1608 TGTGTTTCAAGAAAGTTTCAAGGAGAGGCGCAAGTTATCAAAAACATGTTTCAGAG 1667

QY 2492 AAGGAGCATTAAGTTTACAGCTACAGACAGCTACCAATATCTCTGCTGAGAAACCA 2551

Db 1668 AAGGAGCATTAAGTTTACAGCTACAGACAGCTACCAATATCTCTGCTGAGAAACCA 1727

QY 2552 CAGCATTTTATCTATTTTATTTTAAAGTTTGGTGTCTATCTCTTAATTAAGTTTAA 2611

Db 1728 CAGCATTTTATCTATTTTATTTTAAAGTTTGGTGTCTATCTCTTAATTAAGTTTAA 1787

QY 2612 ATGTCAAAACTGTGACCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 2661

Db 1788 ATGTCAAAACTGTGACCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1837

RESULT 7
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LOCUS BF971929
DEFINITION 602240332F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4329079 5', mRNA sequence.
ACCESSION BF971929
VERSION BF971929
KEYWORDS BF971929.1 GI:12339144
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE NIH-MGC http://mhc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC), Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at: http://image.llnl.gov
Plate: L1CM1189 row: p column: 08

High quality sequence stop: 728.

FEATURES
Location/Qualifiers

1..897
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into pCR2/CMV sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 24.2%; Score 647; DB 2; Length 897;
Best Local Similarity 100.0%; Pred. No. 1.6e-311;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1908 GGGAGCTCCGGAGCTGACCTATCATGATCGGAGAGACATTCCTCCGAGTTGCC 1967
DB 1 GGGAGCTCCGGAGCTGACCTATCATGATCGGAGAGACATTCCTCCGAGTTGCC 60
QY 1968 AGTGGCGGTAAACATCCCGTCTGACTGCTACTGAGGCGGTAACTGCGCACTCAGGTGAA 2027
DB 61 AGTGGCGGTAAACATCCCGTCTGACTGCTACTGAGGCGGTAACTGCGCACTCAGGTGAA 120
QY 2028 AGTCTCACACGCCATGAAATTCATATCTGTGAACAGACAGGTTCAAAAATCTAACG 2087
DB 121 AGTCTCACACGCCATGAAATTCATATCTGTGAACAGACAGGTTCAAAAATCTAACG 180
QY 2088 ATCCAGAGGCGCCGAGACGCTTACACATCGAGGAGAGAGAGCGCTTTTAAATAC 2147
DB 181 ATCCAGAGGCGCCGAGACGCTTACACATCGAGGAGAGAGAGCGCTTTTAAATAC 240
QY 2148 AGAGACAGACAGCTCAAGGTGTTTCAAGCCCCCTGAGGAGAGAGAGAGAGAGGTTCCG 2207
DB 241 AGAGACAGACAGCTCAAGGTGTTTCAAGCCCCCTGAGGAGAGAGAGAGAGAGGTTCCG 300
QY 2208 AAGGTGCTCTGGGAGCTCTTCTGTGAGCTTTTACCTCTGAGTGAAGACCTCTCCC 2267
DB 301 AAGGTGCTCTGGGAGCTCTTCTGTGAGCTTTTACCTCTGAGTGAAGACCTCTCCC 360
QY 2268 AAGAGCCCGGGGGGCGGAGCCGCTCTGTGAGACGCTGGGAGAGGCTCTGTGTGGCA 2327
DB 361 AAGAGCCCGGGGGGCGGAGCCGCTCTGTGAGACGCTGGGAGAGGCTCTGTGTGGCA 420
QY 2328 TCAGCAGCAGAGAGAGAGCTTCTGTAAATGCGGCGCTCCGCGAGAGAGGCGAGTT 2387
DB 421 TCAGCAGCAGAGAGAGAGCTTCTGTAAATGCGGCGCTCCGCGAGAGAGGCGAGTT 480
QY 2388 TGTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAAGTCTGTTTTCAGAGAAAGT 2447
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QY 2448 TTCAGAGGAGAGAGAGAGAGTTTATCAAAAACATGTTTTCAGAGAGAGAGAGT 2507
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QY 2508 ACAGCTTACAGAGAGTACAAATATCTGTCTGTGGAGAAACACAG 2554
DB 601 ACAGCTTACAGAGAGTACAAATATCTGTCTGTGGAGAAACACAG 647

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RESULT 8
CN428709
LOCUS CN428709 755 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000600090657 GRN_PRENEM Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN428709
VERSION CN428709.1 GI:47416303

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 755)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Mura, J., Fisk, G. J.,

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,

Leibowksi, J. and Stanton, L. W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 755 Std Error: 0.00.

Location/Qualifiers

1..755

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/issue_type="embryonic stem cell, retinoic acid and

mitogen-treated hES cell line H7"

/clone_lib="GRN_PRENEM"

/note="Oligo dT primed, full-length enriched cDNA library

from hES cell line H7 (p29) maintained in feeder-free

conditions. Embryoid bodies were generated in the presence

of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 23.9%; Score 640; DB 7; Length 755;
Best Local Similarity 100.0%; Pred. No. 5.2e-308;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2022 GGTGAAGGTCAACAGAGCCATGAATATCATATCTGTGAACAGACAGGTTCAAAA 2081
DB 1 GGTGAAGGTCAACAGAGCCATGAATATCATATCTGTGAACAGACAGGTTCAAAA 60
QY 2082 CTAAGCATCAAGAGCCCTGAGCAGCTTACAGCTGAGAGTGAAGAGAGCGTGTTTTA 2141
DB 61 CTAAGCATCAAGAGCCCTGAGCAGCTTACAGCTGAGAGTGAAGAGAGCGTGTTTTA 120
QY 2142 AATATCAGAGACAGACAGTCAAGGTGTTTCAAGCCCCCTGAGGAGAGAGAGAGAGG 2201
DB 121 AATATCAGAGACAGACAGTCAAGGTGTTTCAAGCCCCCTGAGGAGAGAGAGAGAGG 180
QY 2202 TCTCCGACAGGTGCTCTGAGGAGTACTCTGTGAGAGCTTTTACCTCTGAGTGAACC 2261
DB 181 TCTCCGACAGGTGCTCTGAGGAGTACTCTGTGAGAGCTTTTACCTCTGAGTGAACC 240
QY 2262 CTCGCCAGAGCCCGGGGGGCGGAGCCGCTCTGTGAGAGCGTGGCAGAGGCTCGTG 2321
DB 241 CTCGCCAGAGCCCGGGGGGCGGAGCCGCTCTGTGAGAGCGTGGCAGAGGCTCGTG 300
QY 2322 GTGGCATCAGCAGCAGACAGAGAGCTTCTGTAAATGCGGCGCTCCGCGAGAGAGG 2381
DB 301 GTGGCATCAGCAGCAGACAGAGAGCTTCTGTAAATGCGGCGCTCCGCGAGAGAGG 360
QY 2382 CAGTTTGTCTTTTGTACATTTTCCGAACTACAGTTAAAGCAGAGTCTGTTCAGG 2441
DB 361 CAGTTTGTCTTTTGTACATTTTCCGAACTACAGTTAAAGCAGAGTCTGTTCAGG 420
QY 2442 AAAAGTTTCAAGAGAGAGAGGCAAGTTATCAAAAATGTTTTCAGAGAGAGAGCAT 2501
DB 421 AAAAGTTTCAAGAGAGAGAGGCAAGTTATCAAAAATGTTTTCAGAGAGAGAGCAT 480

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/cissue_type="placenta"
/clone_lib="PLACB1"
/note="Vector: PME18SFL3"

ORIGIN

Query Match 22.4%; Score 600; DB 1; Length 680;
Best Local Similarity 100.0%; Pred. No. 5.2e-288;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1503 CCAAGATTACGTGCTCCCTCTGCAAGAGAGCCGCTGTGCACTGCTGCTTCCAGCC 1562
DB 1 CCAAGATTACGTGCTCCCTCTGCAAGAGAGCCGCTGTGCACTGCTGCTTCCAGCC 60
QY 1563 CATTGCCGAGCCGAGAGCGAGAGCGAGAGAGCCGCGGTGCTCCCTCAGAGAGTGC 1622
DB 61 CATTGCCGAGCCGAGAGCGAGAGCGAGAGAGCCGCGGTGCTCCCTCAGAGAGTGC 120
QY 1623 GGTCTGCTGCAAGCTTTCTGCACTGTAATGAGGCTGCAACCGAGCCGCTGCTAAG 1682
DB 121 GGTCTGCTGCAAGCTTTCTGCACTGTAATGAGGCTGCAACCGAGCCGCTGCTAAG 180
QY 1683 CTGCTGCGCCCGCTTTTGTGAGCTCAACCTGAGTGAAGAGTCTGAGACGCGCTGCTGA 1742
DB 181 CTGCTGCGCCCGCTTTTGTGAGCTCAACCTGAGTGAAGAGTCTGAGACGCGCTGCTGA 240
QY 1743 CAACACAGCTACGAGTCAAGACATCTGAAAGATTACCTGAGCAACAGAGTTGACATG 1802
DB 241 CAACACAGCTACGAGTCAAGACATCTGAAAGATTACCTGAGCAACAGAGTTGACATG 300
QY 1803 GAAAAACATGTTGACCGAGAGCTCTGAGCTCCAGCGGAGAGTCTTCTGCTGTCTGA 1862
DB 301 GAAAAACATGTTGACCGAGAGCTCTGAGCTCCAGCGGAGAGTCTTCTGCTGTCTGA 360
QY 1863 TTACAGAGTCAAGAGAGACACCTGTTGTATCTGCTGTGAGCTTCTGCTGTCTGA 1922
DB 361 TTACAGAGTCAAGAGAGACACCTGTTGTATCTGCTGTGAGCTTCTGCTGTCTGA 420
QY 1923 GCTGACCTATCAGTATCGGAGAGAACTCTGCTTCCAGTTCAGAGTCCAGTCCATATC 1982
DB 421 GCTGACCTATCAGTATCGGAGAGAACTCTGCTTCCAGTTCAGAGTCCAGTCCATATC 480
QY 1983 CCGTCTGAGCTGTAATGAGGCGCTGTAATGCGCAGTCAAGTGAAGTCAACCAAGCAT 2042
DB 481 CCGTCTGAGCTGTAATGAGGCGCTGTAATGCGCAGTCAAGTGAAGTCAACCAAGCAT 540
QY 2043 GAAATTCATCATATCTGTGAACAGACAAAGTTCAAAAATAAGATCCAGAGCCCTGA 2102
DB 541 GAAATTCATCATATCTGTGAACAGACAAAGTTCAAAAATAAGATCCAGAGCCCTGA 600

RESULT 11
BQ215731 870 bp mRNA linear EST 02-MAY-2002
LOCUS BQ215731
DEFINITION AGENCOURT 7549119 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059147
5', mRNA Sequence.
ACCESSION BQ215731
VERSION BQ215731.1 GI:20397131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 870)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcrfemail.nih.gov
Tissue Procurement: DCTD/DIR/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: LIML13325 row: f column: 12
High quality sequence stop: 601.
Location/Qualifiers
1..870

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059147"
/cissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/note="Organ: Lung; Vector: pCW-SORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 21.8%; Score 583; DB 5; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e-279;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 CAACGCGTAGAAATGCCCCAACCCTCCAGAGAGCTGAGAGACAGCGCTGGAGACCA 975
DB 1 CAACGCGTAGAAATGCCCCAACCCTCCAGAGAGCTGAGAGACAGCGCTGGAGACCA 60
QY 976 GACAAAGTAGAGAGAGCGTGAATGATCATCTGTCAGAGACCTGTCAGACATGCTGTG 1035
DB 61 GACAAAGTAGAGAGAGCGTGAATGATCATCTGTCAGAGACCTGTCAGACATGCTGTG 120
QY 1036 AGTTTGACGCTCTGATGACAGCTTCTGCGGCGCTTGTACTCGGCTGATGAGAGCGC 1095
DB 121 AGTTTGACGCTCTGATGACAGCTTCTGCGGCGCTTGTACTCGGCTGATGAGAGCGC 180
QY 1096 TGTGCTGCTGTCTTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1155
DB 181 TGTGCTGCTGTCTTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 1156 AACCACTGTGGAAGATCACTCATTCAGATCCAGACAGAGTTCAGTGAAGAGAT 1215
DB 241 AACCACTGTGGAAGATCACTCATTCAGATCCAGACAGAGTTCAGTGAAGAGAT 300
QY 1216 GTGCAAGTAGATGCGCAGAAATTAATCATCTCAAGACATGCTGACGCCCAAGTCAAG 1275
DB 301 GTGCAAGTAGATGCGCAGAAATTAATCATCTCAAGACATGCTGACGCCCAAGTCAAG 360
QY 1276 CGATCTTTTCTGATGAAGAGAGAGTTCAGAGAGCTGCTGAGCTGTCAGAGCTTAC 1335
DB 361 CGATCTTTTCTGATGAAGAGAGAGTTCAGAGAGCTGCTGAGCTGTCAGAGCTTAC 420
QY 1336 AGTAGAGTCTCAGACATTAGCAGGCATACGTGATGCGGCGAGTGTCTTGAATACAG 1395
DB 421 AGTAGAGTCTCAGACATTAGCAGGCATACGTGATGCGGCGAGTGTCTTGAATACAG 480
QY 1396 AGCAGAGCGGCGCAGCTTCCCACTGCGCAGACACCGAGGCGAGGCGAGAGCCCAAG 1455
DB 481 AGCAGAGCGGCGCAGCTTCCCACTGCGCAGACACCGAGGCGAGGCGAGAGCCCAAG 540
QY 1456 GCCCTGAGGAGTCAACCTCCAGAGTCCGCTGAGCTGACAGAG 1498
DB 541 GCCCTGAGGAGTCAACCTCCAGAGTCCGCTGAGCTGACAGAG 583

RESULT 12
BM459647 916 bp mRNA linear EST 05-FEB-2002
LOCUS BM459647
DEFINITION AGENCOURT 6418058 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534277
5', mRNA Sequence.
ACCESSION BM459647
VERSION BM459647.1 GI:18508687
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS 1 (bases 1 to 916)
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12320 row: h column: 22
 High quality sequence stop: 642.
 Location/Qualifiers
 1..916
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5534277"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN
 Query Match 21.1%; Score 565; DB 4; Length 916;
 Best Local Similarity 100.0%; Pred. No. 1.7e-270;
 Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

709 GGGTCTGGGGGTGGTGGCATCTCCCTAAAGAGAGTGGTCTCTGTGGCAAGTATGA 768
 155 GGGTCTGGGGGTGGTGGCATCTCCCTAAAGAGAGTGGTCTCTGTGGCAAGTATGA 214
 769 GGTCTCAGCTTGGCTCAGCTCTCCAGACAGAAAGAGCGCTCTTGTGCTGGAA 828
 215 GTCTCAGCTTGGCTCAGCTCTCCAGACAGAAAGAGCGCTCTTGTGCTGGAA 274
 829 CCCAGAGATCAGAGAGATTTGAGCCCGTGAAGAGAAATGAGAGAGATGGGACCTT 888
 275 CCCAGAGATCAGAGAGATTTGAGCCCGTGAAGAGAAATGAGAGAGATGGGACCTT 334
 889 GACCTGAAGCGGAGTGTGTGGTGGCAACCGCGTGAAGAAATGCCAAACCGTCCAGG 948
 335 GACCTGAAGCGGAGTGTGTGGTGGCAACCGCGTGAAGAAATGCCAAACCGTCCAGG 394
 949 GACGTGAGAGCGGCGTGGGAAAGCAGACAAAGATGAGAGAGCGTGCATGATCATC 1008
 395 GACGTGAGAGCGGCGTGGGAAAGCAGACAAAGATGAGAGAGCGTGCATGATCATC 454
 455 TGCAGAGACCTGTGACAGCTGCTGAGTTTGCAGCCCTGCATGACAGTTCTGCGG 514
 1009 TGCAGAGACCTGTGACAGCTGCTGAGTTTGCAGCCCTGCATGACAGTTCTGCGG 1068
 515 GCTTGTACTCTCGGCGTGGATGAGAGCGCTGCTGCTGTGCTTACCTGCGCTGCTG 574
 1069 GCTTGTACTCTCGGCGTGGATGAGAGCGCTGCTGCTGTGCTTACCTGCGCTGCTG 1128
 574 GCTTGTACTCTCGGCGTGGATGAGAGCGCTGCTGCTGTGCTTACCTGCGCTGCTG 574
 1129 GACGGGATCTGTAAAAACCATCTCAACCAACCTGTGGAAGCATACCTCCAGCAT 1188
 575 GACGGGATCTGTAAAAACCATCTCAACCAACCTGTGGAAGCATACCTCCAGCAT 634
 1189 CCAGACAAGTGTGAGTGAAGAGATGTGCAAGATGATGATGATGATGATGATGATGAT 1248
 635 CCAGACAAGTGTGAGTGAAGAGATGTGCAAGATGATGATGATGATGATGATGATGAT 694
 1249 CAAGACATGCTGACGCCCAAGTCA 1273

Db 695 CAAGACATGCTGACGCCCAAGTCA 719

RESULT 13
 BMS42545
 LOCUS BMS42545
 DEFINITION BMS42545 1143 bp mRNA linear EST 20-FEB-2002
 AGENCOURT 6426028 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520909
 5', mRNA sequence.
 ACCESSION BMS42545
 VERSION BMS42545.1 GI:18772149
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS 1 (bases 1 to 1143)
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12185 row: k column: 22
 High quality sequence stop: 666.
 Location/Qualifiers
 1..1143
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5520909"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN
 Query Match 21.0%; Score 563; DB 4; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 1.7e-269;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2099 CTGAGACCTTTCAGCACTGAGAGAGAGAGAGCGTGTCTTTAAATACAGACAGCA 2158
 37 CTGAGACCTTTCAGCACTGAGAGAGAGAGAGCGTGTCTTTAAATACAGACAGCA 96
 2159 CGTCAAGGTGTTTTCACAGCCCGCTGAGAGAGAGAGAGCGTGTCTTTAAATACAG 2218
 97 CGTCAAGGTGTTTTCACAGCCCGCTGAGAGAGAGAGAGCGTGTCTTTAAATACAG 156
 2219 GGGGTGACTCTTGTGAGAGCTTTTACCTCTGAGTGAACCTTCCAGAGCGCCGCG 2278
 157 GGGGTGACTCTTGTGAGAGCTTTTACCTCTGAGTGAACCTTCCAGAGCGCCGCG 216
 2279 GGGGTGACTCTTGTGAGAGCTTTTACCTCTGAGTGAACCTTCCAGAGCGCCGCG 2338
 217 GGGGTGACTCTTGTGAGAGCTTTTACCTCTGAGTGAACCTTCCAGAGCGCCGCG 276
 2339 GACGAAGCTTCTGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2398
 277 GACGAAGCTTCTGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
 2399 ACATTTTCGAAATCTAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2458
 337 ACATTTTCGAAATCTAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396

QY 2459 AGGCGAAGTTTATCAAAAATTGTTTCAGAGAGAGGAGCATAGTTTACAGCTTACG 2518
DB 397 AGGCGAAGTTTATCAAAAATTGTTTCAGAGAGAGGAGCATAGTTTACAGCTTACG 456
QY 2519 GACGTACACAATATCTGCTGCTGGGAAAACACACATTTTATCTATTTTATTTTAA 2578
DB 457 GACGTACACAATATCTGCTGCTGGGAAAACACACATTTTATCTATTTTATTTTAA 516
QY 2579 TAGGTTGGTCTTATCTTATTAAGATTTAAATGTCACAACTGTACACAATAATA 2638
DB 517 TAGGTTGGTCTTATCTTATTAAGATTTAAATGTCACAACTGTACACAATAATA 576
QY 2639 TAATTATTAATTTACAAATTGAC 2661
DB 577 TAATTATTAATTTACAAATTGAC 599

RESULT 14
BE407732 666 bp mRNA linear EST 21-JUL-2000
LOCUS 60129777F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629682 5',
DEFINITION mRNA sequence.
ACCESSION BE407732
VERSION BE407732.1 GI:9344182
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 666)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNC316 row: 3 column: 19
High quality sequence stop: 640.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3629682"
/issue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Site-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 20.9%; Score 560; DB 2; Length 666;
Best Local Similarity 99.8%; Freq. No. 5.2e-268;
Matches 610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1156 AACCACTGTGGAACATCTCATCTCAGATCCAGACAAGAGTGCAGTAAGAAGT 1215
DB 1 AACCACTGTGGAACATCTCATCTCAGATCCAGACAAGAGTGCAGTAAGAAGT 60
QY 1216 GTGCAAAAGTATGATCCAGGAATAAATCACTCAAGACATGCTGAGCCCAAGTCAAG 1275
DB 61 GTGCAAAAGTATGATCCAGGAATAAATCACTCAAGACATGCTGAGCCCAAGTCAAG 120

QY 1276 CGGTCTTTTCTGATGAAGAGAGATTTCAGAGACTGCTGAGAGTGTCAAGCGTTGAC 1335
DB 121 CGGTCTTTTCTGATGAAGAGAGATTTCAGAGACTGCTGAGAGTGTCAAGCGTTGAC 180
QY 1336 AGTGAAGTCTGACACATTAGCCAGCATACGTCGTGTGCGGAGTGTCTTAGTACAA 1395
DB 181 AGTGAAGTCTGACACATTAGCCAGCATACGTCGTGTGCGGAGTGTCTTAGTACAA 240
QY 1396 AGGCAAGGCGGAGAGCTCCCACTGCCAGAGCCGAGAGGAGCCAGAGCCCAAG 1455
DB 241 AGGCAAGGCGGAGAGCTCCCACTGCCAGAGCCGAGAGGAGCCAGAGCCCAAG 300
QY 1456 GCCCTGGGAGATGACACCTCTCAAGTCCGTCCAGCTGACAGACAGAGTTCAGT 1515
DB 301 GCCCTGGGAGATGACACCTCTCAAGTCCGTCCAGCTGACAGACAGAGTTCAGT 360
QY 1516 TGCCTCTGCAAGAGAACCCAGCCCTGTGACACTGTCTTCAAGCCATGCCAGCCG 1575
DB 361 TGCCTCTGCAAGAGAACCCAGCCCTGTGACACTGTCTTCAAGCCATGCCAGCCG 420
QY 1576 AAGAGCGAGCGGAGAGAGACCGCGTGTGCGCCCTCAGCAGTGTGCGGTCCGCGAG 1635
DB 421 AAGAGCGAGCGGAGAGAGACCGCGTGTGCGCCCTCAGCAGTGTGCGGTCCGCGAG 480
QY 1636 CCTTCTGCACTGTGATGAGGCTGACACCGGAGCCGCTGCTACAGCTGCGCCCG 1695
DB 481 CCTTCTGCACTGTGATGAGGCTGACACCGGAGCCGCTGCTACAGCTGCGCCCG 540
QY 1696 TTTTGTAGCTCAACCTGTGTGACAGAGTGTGACAGCGGTCTGAACAACAACAGTAC 1755
DB 541 TTTTGTAGCTCAACCTGTGTGACAGAGTGTGACAGCGGTCTGAACAACAACAGTAC 600
QY 1756 GAGTCAGACAT 1766
DB 601 GAGTCAGACAT 611

RESULT 15
AL539797/c 1118 bp mRNA linear EST 24-MAR-2004
LOCUS AL539797 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF031YA23 3-PRIME, mRNA sequence.
ACCESSION AL539797
VERSION AL539797.3 GI:45715435
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1118)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31264360.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6792.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0DF031YA12NP1&c=6792.r.
Location/Qualifiers
1..1118
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF031YA23"

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/issue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

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Query Match      20.1%; Score 539; DB 1; Length 1118;
Best Local Similarity 100.0%; Pred. No. 1.7e-257;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1704 GCTCAACTGGGTGACAGTGTCTGACGCGCGTCTGAAACAACAGCTACGAGTACA 1763
DB 939 GCTCAACTGGGTGACAGTGTCTGACGCGCGTCTGAAACAACAGCTACGAGTACA 880
QY 1764 CATCTGAAGATTAATCTGCGCAACGAGAGTTGACATGGAAGAAAACATGTTGACCGAGG 1823
DB 879 CATCTGAAGATTAATCTGCGCAACGAGAGTTGACATGGAAGAAAACATGTTGACCGAGG 820
QY 1824 CCTCGGTCTCTCAGCGCGGAGTGTCTGCTGTCTGATTAACAGAGTACGCGAGACAC 1883
DB 819 CCTCGGTCTCTCAGCGCGGAGTGTCTGCTGTCTGATTAACAGAGTACGCGAGACAC 760
QY 1884 GCTTCTGTGTAATCTGTGTGCGCTTGCGGAGCTTCCGTGAGCTGACCTATCAGTATCGCA 1943
DB 759 GCTTCTGTGTAATCTGTGTGCGCTTGCGGAGCTTCCGTGAGCTGACCTATCAGTATCGCA 700
QY 1944 GAACATCTCTGCTCCGAGTTCGCAAGTCCGATGCAATCCCGTCCGATGCTTACGAGG 2003
DB 699 GAACATCTCTGCTCCGAGTTCGCAAGTTCGCAATCCCGTCCGATGCTTACGAGG 640
QY 2004 CCGTAACCTCCGCACTCAGGTGAAGCTCACCACGCGCATGAATCATATCATCTGTGA 2063
DB 639 CCGTAACCTCCGCACTCAGGTGAAGCTCACCACGCGCATGAATCATATCATCTGTGA 580
QY 2064 ACAGACAGAGTTCACAAACTAAGCATCAGAGGCGCTTGAGAGCTTTCAGCACTGAGGT 2123
DB 579 ACAGACAGAGTTCACAAACTAAGCATCAGAGGCGCTTGAGAGCTTTCAGCACTGAGGT 520
QY 2124 GAAGAGAGGCTTTTAAATTAATACAGACAGACAGCTGAAGTTCACAGAGGCTT 2183
DB 519 GAAGAGAGGCTTTTAAATTAATACAGACAGACAGCTGAAGTTCACAGAGGCTT 460
QY 2184 GAGGAGAGGAGGAGGAGGCTCTCGACAGAGTGTCTGAGGAGTCTTCTGTGAGCTTT 2242
DB 459 GAGGAGAGGAGGAGGAGGCTCTCGACAGAGTGTCTGAGGAGTCTTCTGTGAGCTTT 401

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RESULT 16      934 bp      mRNA      linear      EST 22-JAN-2001
BF971838
LOCUS          602240424r1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4323076 5',
DEFINITION    mRNA sequence.
ACCESSION     BF971838
VERSION       BF971838.1 GI:12339053
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE     NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE         Unpublished (1999)
JOURNAL       Contact: Robert Strausberg, Ph.D.
              Email: cga9db-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
COMMENT       DNA Sequencing by: Incyte Genomics, Inc.

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FEATURES
source
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4323076"
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/lab_host="RDH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

```

Query Match      19.4%; Score 519; DB 2; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.7e-247;
Matches 639; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1908 GGGCAGCTTCGGTGAAGTGAAGTCACTATCAGTATCGGAGAAACATTCCTGCTCGAGTTGCC 1967
DB 1 GGGCAGCTTCGGTGAAGTGAAGTCACTATCAGTATCGGAGAAACATTCCTGCTCGAGTTGCC 60
QY 1968 AGTGGCCGTAAATCTCCGCTCTGACTGTGAGGCGCGTAATCCGCACTCAGGTGA 2027
DB 61 AGTGGCCGTAAATCTCCGCTCTGACTGTGAGGCGCGTAATCCGCACTCAGGTGA 120
QY 2028 AGCTACCAAGCCATGAATTCATCATCTGTGTAACAGACAGAGTTCAAAACTAAGC 2087
DB 121 AGCTACCAAGCCATGAATTCATCATCTGTGTAACAGACAGAGTTCAAAACTAAGC 180
QY 2088 ATCCAGAGGCGCTGAGAGCTTTCAGACAGTGAAGTGAAGAGGAGGCTTTTAAATAC 2147
DB 181 ATCCAGAGGCGCTGAGAGCTTTCAGACAGTGAAGTGAAGAGGAGGCTTTTAAATAC 240
QY 2148 AGAGACAGACAGTCAAGGTGTTTTCAGAGGCGCTGAGAGGAGGAGGAGGCTTCG 2207
DB 241 AGAGACAGACAGTCAAGGTGTTTTCAGAGGCGCTGAGAGGAGGAGGAGGAGGCTTCG 300
QY 2208 ACAGGTGCTCTGGGTGACCTCTTCTGTGAGAGCTTTTACCCTCTGAGAGACCTCCCC 2267
DB 301 ACAGGTGCTCTGGGTGACCTCTTCTGTGAGAGCTTTTACCCTCTGAGAGACCTCCCC 360
QY 2268 AGAGCCCGGGGGGCGGAGCGCGCTCTGAGAGGCTGAGGAGGAGGCTGAGTGA 2327
DB 361 AGAGCCCGGGGGGCGGAGCGCGCTCTGAGAGGCTGAGGAGGAGGAGGCTGAGTGA 419
QY 2328 TCAGCAGACAGACAGAGCTTCTGTGAACATGCGGCGCTCCGCGAGAGGAGGAGTTT 2387
DB 420 TCAGCAGACAGACAGAGCTTCTGTGAACATGCGGCGCTCCGCGAGAGGAGGAGTTT 479
QY 2388 TGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAAGAGTCTGTTTTCAGGAAAGT 2447
DB 480 TGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAAGAGTCTGTTTTCAGGAAAGT 539
QY 2448 TTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2507
DB 540 TTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 599
QY 2508 ACAGCTTACAGACAGTACACATATCTGCTGCTGGGAAA 2547
DB 600 ACAGCTTACAGACAGTACACATATCTGCTGCTGGGAAA 639

```

RESULT	17
LOCUS	CA916737
DEFINITION	CA916737.1 GI:28951974
ACCESSION	CA916737
VERSION	EST.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 729)
AUTHORS	Scarafia,L.E., Stroufer,S.D. and Swinney,D.C.
TITLE	Identification of Ring Finger proteins that interact with UbcH5A, an ubiquitin-conjugating enzyme
JOURNAL	Unpublished (2002)
COMMENT	Contact: Scarafia LE Enzymology Roche Bioscience 3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA Tel.: 650 354 7997 Fax: 650 354 7554 Email: liliana.scarafia@roche.com Seq primer: matchmaker 5' AD (ctatcgatgatgaagataccacccaacc) POLYA=No
FEATURES	Location/Qualifiers
Source	1..729 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="U5" /cell_type="B cell" /cell_line="EBV-transformed human peripheral blood lymphocyte; B cell population; IG (+)" /lab_host="yeast/B.coli" /clone_1ib="human lymphocyte Matchmaker cDNA library" /note="Vector: pACT; Site 1: XhoI; Site 2: XhoI. Matchmaker yeast two-hybrid system from Clontech;pACT has GAL4 AD under ADHI promoter. This oligo-OT primed library was screened with human UbcH5A as bait, to obtain interacting proteins."
ORIGIN	
Query Match	19.1%; Score 513; DB 6; Length 729;
Best Local Similarity	99.5%; Pred. No. 1.7e-244;
Matches	663; Conservative 0; Pseudomatches 3; Indels 0; Gaps 0;
Oy	560 CGGATCCCCGGGTCCCTCGTGTGAGGCCGCACCTCAGGTGTCCTTGAGGAACAACAGC 619
Dd	13 CCGATCCCCGGGTCCCTCGTGTGAGGCCGCACCTCAGGTGTCCTTGAGGAACAACAGC 72
Oy	620 CATCAACATCGACGTTCAGACCTTTCCCACAGCCTTGAGCTCTTTCACAGAGCTTCTC 679
Dd	73 CATCAACATCGACGTTCAGACCTTTCCCACAGCCTTGAGCTCTTTCACAGAGCTTCTC 132
Oy	680 CTGCGAGGGCGAGAAGGCTTCTTCAGATTGGGTCTGGGGGCTGTGGCATCTTCCCTTAAG 739
Dd	133 CTGCGAGGGCGAGAAGGCTTCTTCAGATTGGGTCTGGGGGCTGTGGCATCTTCCCTTAAG 192
Oy	740 GAAGTGTGCTCCCTGTGGCAAGTAGTAAGTCTCAGGCTTTGGCCCTCACCTCCACAGCA 799
Dd	193 GAAGTGTGCTCCCTGTGGCAAGTAGTAAGTCTCAGGCTTTGGCCCTCACAGCTCCACAGCA 252
Oy	800 GAAAGACTGCGCTCTTTTGTGTGGAACCCACAGATCAGAGGATTTGAGCCCGTGA 859
Dd	253 GAAAGACTGCGCTCTTTTGTGTGGAACCCACAGATCAGAGGATTTGAGCCCGTGA 312
Oy	860 AGAAGAAAATGAGAGAGATGGGGACCTTGACCTGAAGGGCGCATGTTGTTGTCGCAAC 919
Dd	313 AGAAGAAAATGAGAGAGATGGGGACCTTGACCTGAAGGGCGCATGTTGTTGTCGCAAC 372

OY		920	CGCCTAAATAATGCCCAACCGTCCACAGAGACGTCAAGACAGCGCTGGGAAAGCAACA	979
Db		373	CGCCTAATAAATGCCCAAACCGTCCACAGAGACGTCAAGACAGCGCTGGGAAAGCAACA	432
OY		980	AGATGAGAGAGACGCTCATGCATGCATCATCTTGCCAGAGACTTGCTCACGACTGCGTAGATT	1039
Db		433	AGATGAGAGAGACGCTCATGCATGCATCATCTTGCCAGAGAACTGCTCACGACTGCGTAGATT	492
OY		1040	TGCAGCGCTCGATGACACACGTTTCGCGCGGTTGCTACTCGGGGTGATAGAGGCGTCCGT	1099
Db		493	TGCAGCGCTCGATGACACACGTTTCGCGCGGTTGCTACTCGGGGTGATAGAGGCGTCCGT	552
OY		1100	CCCAGTGTCCCTACCTGCGCGCTGTCCCCGTGGAGCGGATCTGTAAAAACCACTCTCAACA	1159
Db		553	CCCAGTGTCCCTACCTGCGCGCTGTCCCCGTGGAGCGGATCTGTAAAAACCACTCTCAACA	612
OY		1160	ACCTGTGGGAAGCATTCCTCATCCAGATCCAGACAAAGAAGTCGATGGAGTAAGAGATGTGC	1219
Db		613	ACCTGTGGGAAGCATTCCTCATCCAGATCCAGACAAAGAAGTCGATGGAGTAAGAGATGTGC	672
OY		1220	AAAGTA 1225	
Db		673	AAAGTA 678	
RESULT 18				
LOCUS	BE280165	690 bp	mRNA	linear EST 13-JUL-2000
DEFINITION	60115837OP1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504928 5', mRNA sequence.			
ACCESSION	BE280165			
VERSION	BE280165.1	GI:9155072		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov Plate: LNCM80 row: 1 column: 17 High quality sequence stop: 626. Location/Qualifiers 1. 690 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cd_name="IMAGE:3504928" /tissue_type="choriocarcinoma" /lab_host="DH10B (phage-resistant)" /clone_id="NIH_MGC_21" /note="Organ: placenta; Vector: pOT87; Site:1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. directionally cloned into RscBI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."			
FEATURES				
Source				
Query Match	18.2%; Score 488; DB 2; Length 690;			
Best Local Similarity	99.8%; Pred. No. 5.3e-232;			

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6380102"
/issue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_40"
/note="Organ: prostate; Vector: pORF7, Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

Query Match 17.8%; Score 478; DB 5; Length 910;
Best Local Similarity 100.0%; Pred. No. 5.3e-227;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GCCGCAATGCTCTTGAACAGCGCGCGGCGGCGGCTTCCGGTTCCGGCGCGCGCGCG 76
DB 10 GCCGCAATGCTCTTGAACAGCGCGCGGCGGCGGCGGCTTCCGGTTCCGGCGCGCG 69
QY 77 GGATGTGAATCCCGATGAGCGCGCCGAGAGGCAAGCATGTCGCCCGCGCGCAACCTT 136
DB 70 GGATGTGAATCCCGATGAGCGCGCCGAGAGGCAAGCATGTCGCCCGCGCGCAACCTT 129
QY 137 GGGGACGGCTCTGCGTCTGGCGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 196
DB 130 GGGGACGGCTCTGCGTCTGGCGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 189
QY 197 GGGAGTGAACCATCGGCGGAGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
DB 190 GGGAGTGAACCATCGGCGGAGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 249
QY 257 TCTCTGAGATCACTGTAGATTGTAGTGGATGATAAATCAGTCAAGTGAACCTGGAAG 316
DB 250 TCTCTGAGATCACTGTAGATTGTAGTGGATGATAAATCAGTCAAGTGAACCTGGAAG 309
QY 317 ATACCAAGCAGCTGGAACAGTGAATTAACAAGTTGTTAAGAAAGCAAGATGCC 376
DB 310 ATACCAAGCAGCTGGAACAGTGAATTAACAAGTTGTTAAGAAAGCAAGATGCC 369
QY 377 CTTTACAGCTGGGAGTGTCTATCTTGTGTGACGAAAGATGAACCGGAACAAG 436
DB 370 CTTTACAGCTGGGAGTGTCTATCTTGTGTGACGAAAGATGAACCGGAACAAG 429
QY 437 TGGCATACCTCTATGATCTTTAAGTGAAGCAAGGATGACACAGATCTTTGA 494
DB 430 TGGCATACCTCTATGATCTTTAAGTGAAGCAAGGATGACACAGATCTTTGA 487

RESULT 21

LOCUS BQ887242 938 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8670262 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6380588
5', mRNA sequence.

ACCESSION BQ887242
VERSION BQ887242.1 GI:22279256
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 938)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2569 row: 9 column: 21
High quality sequence stop: 572.
Location/Qualifiers
1. 938

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6380588"
/issue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_40"
/note="Organ: prostate; Vector: pORF7, Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.8%; Score 478; DB 5; Length 938;
Best Local Similarity 100.0%; Pred. No. 5.3e-227;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GCCGCAATGCTCTTGAACAGCGCGCGGCGGCGGCTTCCGGTTCCGGCGCGCGCG 76
DB 10 GCCGCAATGCTCTTGAACAGCGCGCGGCGGCGGCGGCTTCCGGTTCCGGCGCGCG 69
QY 77 GGATGTGAATCCCGATGAGCGCGCCGAGAGGCAAGCATGTCGCCCGCGCGCAACCTT 136
DB 70 GGATGTGAATCCCGATGAGCGCGCCGAGAGGCAAGCATGTCGCCCGCGCGCAACCTT 129
QY 137 GGGGACGGCTCTGCGTCTGGCGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 196
DB 130 GGGGACGGCTCTGCGTCTGGCGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 189
QY 197 GGGAGTGAACCATCGGCGGAGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
DB 190 GGGAGTGAACCATCGGCGGAGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 249
QY 257 TCTCTGAGATCACTGTAGATTGTAGTGGATGATAAATCAGTCAAGTGAACCTGGAAG 316
DB 250 TCTCTGAGATCACTGTAGATTGTAGTGGATGATAAATCAGTCAAGTGAACCTGGAAG 309
QY 317 ATACCAAGCAGCTGGAACAGTGAATTAACAAGTTGTTAAGAAAGCAAGATGCC 376
DB 310 ATACCAAGCAGCTGGAACAGTGAATTAACAAGTTGTTAAGAAAGCAAGATGCC 369
QY 377 CTTTACAGCTGGGAGTGTCTATCTTGTGTGACGAAAGATGAACCGGAACAAG 436
DB 370 CTTTACAGCTGGGAGTGTCTATCTTGTGTGACGAAAGATGAACCGGAACAAG 429
QY 437 TGGCATACCTCTATGATCTTTAAGTGAAGCAAGGATGACACAGATCTTTGA 494
DB 430 TGGCATACCTCTATGATCTTTAAGTGAAGCAAGGATGACACAGATCTTTGA 487

RESULT 22

LOCUS BM541730 1092 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6439229 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531628
5', mRNA sequence.

ACCESSION BM541730
VERSION BM541730.1 GI:18770627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Db 618 GGACGAGGGTCTCCGACAGTCTCTGGGGGTGACTTCTGTGAGACT 666

RESULT 24
LOCUS AU132825 824 bp mRNA linear EST 01-AUG-2002
DEFINITION AU132825 NT2RP4 Homo sapiens cDNA clone NT2RP4000648 5', mRNA sequence.
ACCESSION AU132825
VERSION AU132825
KEYWORDS AU132825.1 GI:10993364
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 824)
AUTHORS Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Maehuo,Y. and Isogai,T.
TITLE HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Maehuo,Y., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
LOCATION/Qualifiers
1. 824
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP4000648"
/tissue_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP4"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 17.5%; Score 468; DB 1; Length 824;
Best Local Similarity 100.0%; Pred. No. 5.3e-222; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 CTCTTGACAGCGCGCGCGCGAGCCGCTTCGCGGTTCCGCGCGCGGAGATGTGAAT 86
1 CTCTTGACAGCGCGCGCGCGAGCCGCTTCGCGGTTCCGCGCGCGGAGATGTGAAT 60

Qy 87 CCCGATGAGCGCGCGCGCGAGGAGCAAGATGCCCGCGCGAGCCCTTGCGGACGGCT 146
61 CCCGATGAGCGCGCGCGAGGAGCAAGATGCCCGCGCGAGCCCTTGCGGACGGCT 120

Db 147 CCTGAGTCTGGGCGCGGAGGAGGCGAGCGCAGCGTCTCTGAGGAGACGGGAGTGAAC 206
121 CCTGAGTCTGGGCGCGGAGGAGGCGAGCGCAGCGTCTCTGAGGAGACGGGAGTGAAC 180

Qy 207 CATCGGGCGAGACGAGGTTGCGACTTCTCTCCCAAGCAATTAATGCTCTTGAGA 266
181 CATCGGGCGAGACGAGGTTGCGACTTCTCTCCCAAGCAATTAATGCTCTTGAGA 240

Qy 267 TCACCTGTAGAAATTTAGTGTGAGTGAATTAATCAGGTCACTGAGAAATACAGCAC 326
241 TCACCTGTAGAAATTTAGTGTGAGTGAATTAATCAGGTCACTGAGAAATACAGCAC 300

Db 327 CAGTGAACAGTGAATTAACAGCTGAAGGTGTTAAGAGAGAGACATGCCCTTTACAGAC 386

Db 301 CAGTGAACAGTGAATTAACAGCTGAAGGTGTTAAGAGAGAGACATGCCCTTTACAGAC 360

Qy 387 TGGGATGTCACTTACTTGGTGTACAGAAATGAACCGGAACACACAGCTGCATACCT 446
361 TGGGATGTCACTTACTTGGTGTACAGAAATGAACCGGAACACACAGCTGCATACCT 420

Qy 447 CTATGAATCTTTAAGTGAAGAAAGCAGTGAACAAAGAAATCCTTTGA 494
421 CTATGAATCTTTAAGTGAAGAAAGCAGTGAACAAAGAAATCCTTTGA 468

RESULT 25
LOCUS BE257482 712 bp mRNA linear EST 13-JUL-2000
DEFINITION BE257482 60111439F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352136 5', mRNA sequence.
ACCESSION BE257482
VERSION BE257482
KEYWORDS BE257482.1 GI:9127957
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaab@ncl.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: image.liml.gov.
Plate: LIM150 row: n column: 09
High quality sequence stop: 571.
LOCATION/Qualifiers
1. 712
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3352136"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 16"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 17.0%; Score 456; DB 2; Length 712;
Best Local Similarity 99.8%; Pred. No. 5.3e-216; Indels 1; Gaps 0;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1313 TCTTGAGCTGTCAAGCTTGAAGTGAAGTCTTCAAGCAATTAAGCAAGCAATGCTGT 1372
1 TCTTGAGCTGTCAAGCTTGAAGTGAAGTCTTCAAGCAATTAAGCAAGCAATGCTGT 60

Qy 1373 GCCGCGAGTGTCTAGTGAAGAGGAGGCGGCGAGCGTCCGACGCGGAGACCG 1432
61 GCCGCGAGTGTCTAGTGAAGAGGAGGCGGCGAGCGTCCGACGCGGAGACCG 120

Qy 1433 AGGGGAGACGAGAGCCCAAGGCGCTGGGGAGTGAACCTTCAAGTCCGACGCTGA 1492
121 AGGGGAGACGAGAGCCCAAGGCGCTGGGGAGTGAACCTTCAAGTCCGACGCTGA 180

RESULT	26					
LOCUS	BG335362					
DEFINITION	BG335362	1096 bp	mRNA	linear	EST 27-FEB-2001	
	6024041922.1	NIH_MGC_21	Homo sapiens	CDNA clone	IMAGE:4541638 5'	
ACCESSION	BG335362					
VERSION	BG335362					
KEYWORDS	BG335362.1	GI:13141800				
SOURCE	EST.					
ORGANISM	Homo sapiens	(human)				
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 1096)					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					

Location/Qualifiers
1. .1096

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/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH1 MGC 21"
/notes="Organ: Placenta; Vector: pOMB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAACGAG(c). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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RESULT	27					
LOCUS	BMS58904					
DEFINITION	BMS58904	1022 bp	mRNA	linear	EST-20-FEB-2007	
AGNCOURT	6562815 NIH_MGC_67	Homo sapiens	CDNA clone	IMAGE:551112		
ACCESSION	BMS58904					
VERSION	BMS58904.1	GI:18802039				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 1022)					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					

Location/Qualifiers
1. .1022

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:551112"
/tissue_type="retinoblastoma"

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ORIGIN

/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 Kb. Library constructed by Life
Technologies."

Query Match 16.9%; Score 452; DB 4; Length 1022;
Best Local Similarity 100.0%; Pred. No. 5.3e-214;
Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GGGTCTGGGGGTGGGTCATCTCCCTAAAGAAAGTGTCTCTGTGGCAAGTGA 768
DB 150 GGGTCTGGGGGTGGGTCATCTCCCTAAAGAAAGTGTCTCTGTGGCAAGTGA 209
QY 769 GTCTCAAGCTTTGCTCTGAGCTCTCCAGACAGAAAGCTGCTTTTGTCTGGAA 828
DB 210 GTCTCAAGCTTTGCTCTGAGCTCTCCAGACAGAAAGCTGCTTTTGTCTGGAA 269
QY 829 CCCAGAGATCAGAGAGATTGGAGCCCGTGAAGAAATGAGAGAGATGGGGACCTT 888
DB 270 CCCAGAGATCAGAGAGATTGGAGCCCGTGAAGAAATGAGAGAGATGGGGACCTT 329
QY 889 GACCTGAACGGGAGATTGTGTGTGCACAACCGCTGAGAAATGCCAAACCTGTCAAG 948
DB 330 GACCTGAACGGGAGATTGTGTGTGCACAACCGCTGAGAAATGCCAAACCTGTCAAG 389
QY 949 GACCTGAACGGGAGATTGTGTGTGCACAACCGCTGAGAAATGCCAAACCTGTCAAG 1008
DB 390 GACCTGAACGGGAGATTGTGTGTGCACAACCGCTGAGAAATGCCAAACCTGTCAAG 449
QY 1009 TGGCAGAGACTGTGACAGACTGGTGTGAGCTTCCAGCCCTGACAGACACTCTCCGCG 1068
DB 450 TGGCAGAGACTGTGACAGACTGGTGTGAGCTTCCAGCCCTGACAGACACTCTCCGCG 509
QY 1069 GCTTGTACTCTGGGCTGAGTGAAGCGCTCGTCCCTGTGCTCACTGCGCTGCTCCGCTG 1128
DB 510 GCTTGTACTCTGGGCTGAGTGAAGCGCTCGTCCCTGTGCTCACTGCGCTGCTCCGCTG 569
QY 1129 GAGCGGATCTGTAAAAACCAATCTCAACAA 1160
DB 570 GAGCGGATCTGTAAAAACCAATCTCAACAA 601
RESULT 28
BO936072 953 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8779684 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6371968
DEFINITION 5', mRNA sequence.
ACCESSION BO936072
VERSION BO936072.1 GI:22351455
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 953)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DIR/Gaardar
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2546 row: p column: 17
High quality sequence stop: 630.
Location/Qualifiers

source

1..953
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6371968"
/clone_lib="NIH_MGC_18"
/note="Organ: Lung; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

Query Match 16.8%; Score 450; DB 5; Length 953;
Best Local Similarity 100.0%; Pred. No. 5.3e-213;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GCGCAGCCGGTTCGGGTTTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGA 104
DB 1 GCGCAGCCGGTTCGGGTTTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGA 60
QY 105 GGAAGGCAAGCAAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 164
DB 61 GGAAGGCAAGCAAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 165 GGAAGGCAAGCAAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 224
DB 121 GGAAGGCAAGCAAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 225 TTGCGACCTTTCTTCCCGACAAATTAATCTGTCTGAGATCACTGAAATTTAGT 284
DB 181 TTGCGACCTTTCTTCCCGACAAATTAATCTGTCTGAGATCACTGAAATTTAGT 240
QY 285 GATGAAAAATCAGGTCAAGTGAACATGGAATTAACACACAGTGGAAAGTGAATTA 344
DB 241 GATGAAAAATCAGGTCAAGTGAACATGGAATTAACACACAGTGGAAAGTGAATTA 300
QY 345 CAAGCTGAAGTTGTTAAGAGAGACATGCTCTTAAGACATGCGGATGTCTACTT 404
DB 301 CAAGCTGAAGTTGTTAAGAGAGACATGCTCTTAAGACATGCGGATGTCTACTT 360
QY 405 GGTGTACAGAAAGATGAACCGGAACAAAGTGGATTAATCTTAAGTGA 464
DB 361 GGTGTACAGAAAGATGAACCGGAACAAAGTGGATTAATCTTAAGTGA 420
QY 465 AAAGCAAGGATGACCAAGAAATCTTTGA 494
DB 421 AAAGCAAGGATGACCAAGAAATCTTTGA 450
RESULT 29
BO924736 938 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT 8853777 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374110
DEFINITION 5', mRNA sequence.
ACCESSION BO924736
VERSION BO924736.1 GI:22339767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 938)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2552 row: 1 column: 23
 High quality sequence scop: 629.
 Location/Qualifiers

FEATURES

source

1..938
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6374110"
 /issue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 16.7%; Score 447; DB 5; Length 938;

Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

48 CAGCCGGTTCGGGTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGAGGA 107
 1 CAGCCGGTTCGGGTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGAGGA 60
 108 AGGCAAGCAGTGGCCCGCCGAGCCCTGGGAGCGGCTTCCTGCTGGGCGGAGGA 167
 61 AGGCAAGCAGTGGCCCGCCGAGCCCTGGGAGCGGCTTCCTGCTGGGCGGAGGA 120
 168 GGGCGGCGGAGCTCTCTGAGAAAGGGAGTGAACATCGGCGGAGGACGAGGTTG 227
 121 GGGCGGCGGAGCTCTCTGAGAAAGGGAGTGAACATCGGCGGAGGAGAGGTTG 180
 228 CGACCTTCTCTCCCGAGCAATTAATCTGCTCTGAGATCACTGTAAATTGTAGTGA 287
 181 CGACCTTCTCTCCCGAGCAATTAATCTGCTCTGAGATCACTGTAAATTGTAGTGA 240
 288 TGAATAATCAAGTCAAGTGAACACTGGAAGTACAGACCAAGTGAACAGTATTACAA 347
 241 TGAATAATCAAGTCAAGTGAACACTGGAAGTACAGACCAAGTGAACAGTATTACAA 300
 348 GGTGAAGGTGTTAAGAGAGACATGCCCTTACAGACTGGGGAGTGTACTACTTGGT 407
 301 GGTGAAGGTGTTAAGAGAGACATGCCCTTACAGACTGGGGAGTGTACTACTTGGT 360
 408 GTACAGGAAGATGAACCGGAACACAAGTGGCATCTCTAATGAATCTTTAAGTAAAA 467
 361 GTACAGGAAGATGAACCGGAACACAAGTGGCATCTCTAATGAATCTTTAAGTAAAA 420
 468 GCAAGGCATGACACAAGATCTTTTGA 494
 421 GCAAGGCATGACACAAGATCTTTTGA 447

Db

RESULT 30

BX486289

LOCUS BX486289 535 bp mRNA linear EST 04-SEP-2003

DEFINITION DKFZp686P03250.r1 686 (synonym: h1cc3) Homo sapiens cDNA clone

ACCESSION

VERSION BX486289.1 GI:31949829

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 535)

AUTHORS

Bloecker,H., Boecker,M., Mewes,H.W., Well,B., Amid,C., Oanger,A.,

TITLE

EST (Bloecker,H., Boecker,M., Mewes,H.W., Well,B., Amid,C., et al.)

JOURNAL

Unpublished (2003)

COMMENT

Contact: MIPS

FEATURES

source

1..535
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686P03250"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="686 (synonym: h1cc3)"
 /note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;
 cDNA-collection"

ORIGIN

Query Match

Best Local Similarity 16.3%; Score 436; DB 5; Length 535;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

59 GGGTTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGAGGAGCAAGCACT 118
 2 GGGTTCGGCGCGGGGAGTGAATCCGATGAGCGGCCGAGGAGCAAGCACT 61
 119 GGGCGCCGCGGAGCCCTGGGAGCGGCTTCCTGCTGGGCGGAGGAGCCGCG 178
 62 GGGCGCCGCGGAGCCCTGGGAGCGGCTTCCTGCTGGGCGGAGGAGCCGCG 121
 179 AGTCTCTCTGAGAAAGGGAGTGAACATCGGCGGAGGAGGAGGTTCCACTTCT 238
 122 AGTCTCTCTGAGAAAGGGAGTGAACATCGGCGGAGGAGGAGGTTCCACTTCT 181
 239 TCCCGAGCAATTAATCTGCTCTGAGATCACTGTAAATTGTAGTGAATAATCAG 298
 182 TCCCGAGCAATTAATCTGCTCTGAGATCACTGTAAATTGTAGTGAATAATCAG 241
 299 GTCAAGTCACTGGAAGTACAGACCAAGTGAACAGTATTACAAAGCTGAAGTTG 358
 242 GTCAAGTCACTGGAAGTACAGACCAAGTGAACAGTATTACAAAGCTGAAGTTG 301
 359 TTAAGAGAGACATGCCCTTACAGACTGGGGAGTGTACTACTTGGTGTACAGAGAG 418
 302 TTAAGAGAGACATGCCCTTACAGACTGGGGAGTGTACTACTTGGTGTACAGAGAG 361
 419 ATGAACCGGAACACAAGTGGCATCTCTAATGAATCTTTAAGTAAAAAGCAAGCATGA 478
 362 ATGAACCGGAACACAAGTGGCATCTCTAATGAATCTTTAAGTAAAAAGCAAGCATGA 421
 479 CACAAGATCTTTTGA 494
 422 CACAAGATCTTTTGA 437

RESULT 31

BX486564
 LOCUS BX486564 557 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZp686H04252_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 ACCESSION BX486564
 VERSION BX486564.1 GI:31950352
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 557)
 AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Pobo, G., Han, M. and Wiemann, S.
 EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
 TITLE Unpublished (2003)
 JOURNAL Contact: MIPS
 COMMENT MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 clone from S. Wiemann. Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 31 sequence available.
 This clone (DKFZp686H04252) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES

source
 1. 557
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686H04252"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="686 (synonym: hlcc3)"
 /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB; cDNA-collection"

ORIGIN

Query Match 16.3%; Score 436; DB 5; Length 557;
 Best Local Similarity 100.0%; Pred. No. 5.3e-206;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 GGGTTGGGCGGGGGGGGATGTGAATCCCGATGAGCGGCCCGGAGAAAGCGAAGCT 118
 DB 2 GGGTTGGGCGGGGGGGGATGTGAATCCCGATGAGCGGCCCGGAGAAAGCGAAGCT 61
 QY 119 CGGCGCGCGCGGAGCCCTGGGAGCGGCTCTGAGTCTGGGCGGGGAGGAGGCGGAGCCCG 178
 DB 62 CGGCGCGCGCGGAGCCCTGGGAGCGGCTCTGAGTCTGGGCGGGGAGGAGGCGGAGCCCG 121
 QY 179 AGCTCTCTCTGAGAAAGCGGAGTGCATCGGCGCGGAGAGCGAGGTTGGCACTTTCT 238
 DB 122 AGCTCTCTCTGAGAAAGCGGAGTGCATCGGCGCGGAGAGCGAGGTTGGCACTTTCT 181
 QY 239 TCCCGAGCAATAACTGCTCTGAGATCACTGTGAATTTGATGATGAAAAATCAG 298
 DB 182 TCCCGAGCAATAACTGCTCTGAGATCACTGTGAATTTGATGATGAAAAATCAG 241
 QY 299 GTCAGGTGACATCGAAGATACAGACACGAGTGAACAGTGAATTAAGCTGAAGTTG 358
 DB 242 GTCAGGTGACATCGAAGATACAGACACGAGTGAACAGTGAATTAAGCTGAAGTTG 301
 QY 359 TTAAGAGCAGACATGCCCTTTTACAGCTGGGAGTGCATCTTGTGTGTACAGAGA 418
 DB 302 TTAAGAGCAGACATGCCCTTTTACAGCTGGGAGTGCATCTTGTGTGTACAGAGA 361
 QY 419 ATGAACCGGAACAACGTGGCATCTCTATGAATCTTTAAGTGAAGCAAGGCAATGA 478
 DB 362 ATGAACCGGAACAACGTGGCATCTCTATGAATCTTTAAGTGAAGCAAGGCAATGA 421

QY 479 CACAGAAATCTTTGA 494
 DB 422 CACAGAAATCTTTGA 437

RESULT 32
 LOCUS CB989147
 DEFINITION AGENCOURT 13891036 NIH MGC_147 Homo sapiens cDNA clone
 ACCESSION CB989147
 VERSION CB989147.1 GI:30283667
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 811)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Haneson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: http://image.llnl.gov
 Plate: NDM375 row: 1 column: 17
 High quality sequence stop: 476.

FEATURES

source
 1. 811
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAG:30342520"
 /issue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_1ib="NIH MGC 147"
 /note="Organ: Placenta; Vector: pBluescript; Site 1: all-XhoI; Site 2: BamH; Oligo-dr primed using primer 5'-TTTCTTTTCTTTTCTT-3', size-selected for average insert size 2.3 kb and normalized to RCT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH-MGC library."

ORIGIN

Query Match 16.2%; Score 435; DB 6; Length 811;
 Best Local Similarity 100.0%; Pred. No. 1.7e-205;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 GGTTCGCGCGGCGGAGTGAATCCGATGAGCGGCCCGGAGAAAGCGAAGCAATG 119
 DB 27 GGTTCGCGCGGCGGAGTGAATCCGATGAGCGGCCCGGAGAAAGCGAAGCAATG 86
 QY 120 GCCGCGCGCGGAGCCCTGGGAGCGGCTCTGAGTCTGGGCGGGGAGAGGCGGAG 179
 DB 87 GCCGCGCGCGGAGCCCTGGGAGCGGCTCTGAGTCTGGGCGGGGAGAGGCGGAG 146
 QY 180 CTTCTCTCTGAGAAAGCGGAGTGCATCGGCGCGGAGACAGAGTTGGCACTTTCTT 239
 DB 147 CTTCTCTCTGAGAAAGCGGAGTGCATCGGCGCGGAGACAGAGTTGGCACTTTCTT 206
 QY 240 CCCGAGCAATAACTGCTCTGAGATCACTGTGAATTTGATGATGAAAAATCAG 299
 DB 207 CCCGAGCAATAACTGCTCTGAGATCACTGTGAATTTGATGATGAAAAATCAG 266

QY 300 TCAGGTGAACCTGGAAGATACCAAGCACAGTGGAAAGATGATTAAACAGCTGAAGTTCT 359
 |||||
 DB 267 TCAGGTGAACCTGGAAGATACCAAGCACAGTGGAAAGATGATTAAACAGCTGAAGTTCT 326
 |||||
 QY 360 TAAGAAGCAGATGCGCTTTACAGACTGGGATGTCATCTAATTGGTGTACAGGAAGA 419
 |||||
 DB 327 TAAGAAGCAGATGCGCTTTACAGACTGGGATGTCATCTAATTGGTGTACAGGAAGA 386
 |||||
 QY 420 TGAACCGGAACAACAAGTGGCATACCTCTATGATCTTTAAGTGAAGAACCAAGGATGAC 479
 |||||
 DB 387 TGAACCGGAACAACAAGTGGCATACCTCTATGATCTTTAAGTGAAGAACCAAGGATGAC 446
 |||||
 QY 480 ACAAGATCTTTGA 494
 |||||
 DB 447 ACAAGATCTTTGA 461
 |||||

RESULT 33
 CB961597 806 bp mRNA linear EST 29-APR-2003
 LOCUS CB961597
 DEFINITION AGENCOURT_13892092 NIH_MGC_148 Homo sapiens cDNA clone
 IMAGE:30337709 5', mRNA sequence.
 CB961597
 ACCESSION CB961597.1 GI:30217714
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 806)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgrabbs-rc@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM363 row: d column: 06
 High quality sequence stop: 542.
 Location/Qualifiers
 1..806
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30337709"
 /issue_type="pre-clampic placenta"
 /lab_host="DH10B TONa"
 /clone_id="NIH_MGC_148"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 all-chor; Site_2: BamI; Library is oligo-dT primed and
 directionally cloned using primer
 5'-TTTTTTTCTTTTCTT-3', size-selected for average insert
 size 2.3 kb and normalized to ROP 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NIH/NHGRI, in
 National Institutes of Health). Note: this is a NIH-MGC
 library."

ORIGIN

Query Match 16.2%; Score 433; DB 6; Length 806;
 Best Local Similarity 100.0%; Pred.No.17e-204;
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 TTCGGCGCGGGCGGAGATGTGATCCGATGAGCGGCGGAGAGCAAGCAAGTCCG 121
 |||||
 DB 29 TTCGGCGCGGGCGGAGATGTGATCCGATGAGCGGCGGAGAGCAAGCAAGTCCG 88
 |||||

QY 122 GCGCGCGCGAGCCTCTGGGAGAGGCTCTGCGCTCTGGGCGCGGAGAGGCGGCGGACG 181
 |||||
 DB 89 GCGCGCGCGAGCCTCTGGGAGAGGCTCTGCGCTCTGGGCGCGGAGAGGCGGCGGACG 148
 |||||
 QY 182 TCCTCTGAGGAGGCGGAGTGGACCATGGGCGGAGAGGTTGGACCTTCTCTCC 241
 |||||
 DB 149 TCCTCTGAGGAGGCGGAGTGGACCATGGGCGGAGAGGTTGGACCTTCTCTCC 208
 |||||
 QY 242 CCAGCAATTAACCTGCTCTGGAAGATCACTGATGATTTAGTGGATGAAAAATCAGGTC 301
 |||||
 DB 209 CCAGCAATTAACCTGCTCTGGAAGATCACTGATGATTTAGTGGATGAAAAATCAGGTC 268
 |||||
 QY 302 AGGTGACCTGGAAGATACCAAGCACCAGTGGAAAGATTAACAGCTGAAGGTTGTA 361
 |||||
 DB 269 AGGTGACCTGGAAGATACCAAGCACCAGTGGAAAGATTAACAGCTGAAGGTTGTA 328
 |||||
 QY 362 AGAAGCAGACATGCGCTTTACAGACTGGGAGATGTCATCTGCTGTCAGAGGAATG 421
 |||||
 DB 329 AGAAGCAGACATGCGCTTTACAGACTGGGAGATGTCATCTGCTGTCAGAGGAATG 388
 |||||
 QY 422 AACCGGAACAACAAGTGGCATACCTCTATGATCTTTAAGTGAAGAACCAAGGATGACAC 481
 |||||
 DB 369 AACCGGAACAACAAGTGGCATACCTCTATGATCTTTAAGTGAAGAACCAAGGATGACAC 448
 |||||
 QY 482 AAGATCTCTTGA 494
 |||||
 DB 449 AAGATCTCTTGA 461
 |||||

RESULT 34
 AU154212/c 518 bp mRNA linear EST 05-AUG-2002
 LOCUS AU154212
 DEFINITION NT2RP4 Homo sapiens cDNA clone NT2RP400455 3', mRNA
 sequence.
 AU154212
 ACCESSION AU154212.1 GI:11015733
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 518)
 Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
 Ozawa,M., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuno,Y.
 and Isogai,T.
 HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
 Saito,K., Yamamoto,J., Ozawa,M., Nishikawa,T., Nakamura,Y.,
 Nagai,T., Sugano,S., Masuno,Y., Isogai,T.)
 Unpublished (2000)
 CONTACT: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..518
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RP4000455"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_id="NT2RP4"
 /note="Vector: pMT186FL3; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 15.9%; Score 426; DB 1; Length 518;
 Best Local Similarity 99.8%; Pred. No. 5.3e-201;
 Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2185 AAGGAAGGAGCGAGGGGTCTCCGACAGGTCTCTGGGGTACTCTTCTGTGAGCTTTT 2244
 DB 503 AAGGAAGGAGCGAGGGGTCTCCGACAGGTCTCTGGGGTACTCTTCTGTGAGCTTTT 444
 QY 2245 ACCCTTGAAGTGAAGCCCTTCCGAGAGCCCGGGGGCCGAGGCCCTCTCTGTGAGC 2304
 DB 443 ACCCTTGAAGTGAAGCCCTTCCGAGAGCCCGGGGGCCGAGGCCCTCTCTGTGAGC 384
 QY 2305 GCTGGCAGGGCTCGTGTGTGATGACAGCAGAGCGAAGCCTTCTGTGAACATGCGG 2364
 DB 383 GCTGGCAGGGCTCGTGTGTGATGACAGCAGAGCGAAGCCTTCTGTGAACATGCGG 324
 QY 2365 CGTCCCGCGAGAGGGGAGTTTGTCTTTTGTACATTTCCGAAACTACAGTTAAAGC 2424
 DB 323 CGTCCCGCGAGAGGGGAGTTTGTCTTTTGTACATTTCCGAAACTACAGTTAAAGC 264
 QY 2425 AGAAGTCTGTTTCAAGAAAAAGTTTCAAGGAGAGGGCAAGTTTATCAAAAACATTGTT 2484
 DB 263 AAAAGTCTGTTTCAAGAAAAAGTTTCAAGGAGAGGGCAAGTTTATCAAAAACATTGTT 204
 QY 2485 TCAGAGGAAGGAGCATTAAGTTTACAGCCTACAGAGCGTACCAATATCCTGCTGGG 2544
 DB 203 TCAGAGGAAGGAGCATTAAGTTTACAGCCTACAGAGCGTACCAATATCCTGCTGGG 144
 QY 2545 AAAACACAGCATTATATCTTTTATTTTATTTTATAGTTTGGTCTTATCTTCAATA 2604
 DB 143 AAAACACAGCATTATATCTTTTATTTTATTTTATAGTTTGGTCTTATCTTCAATA 84
 QY 2605 GATTTAATGTCAAACTGTAGCACAATAATATTAATTATTAACAATTGAC 2661
 DB 83 GATTTAATGTCAAACTGTAGCACAATAATATTAATTATTAACAATTGAC 27

RESULT 35
 AUI38310 687 bp mRNA linear EST 02-AUG-2002
 LOCUS AUI38310 PLACE1 Homo sapiens cDNA clone PLACE1008304 5', mRNA
 DEFINITION sequence.
 AUI38310
 ACCESSION AUI38310.1 GI:10999831
 VERSION AUI38310.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 687)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Nakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Isegai, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isegai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute
 FEATURES
 source
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="PLACE1008304"

Query Match 15.7%; Score 421; DB 1; Length 687;
 Best Local Similarity 99.8%; Pred. No. 1.7e-198;
 Matches 471; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 720 TGGTGGCATCTCCCTTAAGGAAGTGTCCCTCTGTGGCAATGATGAAGTTCAGACTT 779
 DB 1 TGGTGGCATCTCCCTTAAGGAAGTGTCCCTCTGTGGCAATGATGAAGTTCAGACTT 60
 QY 780 TGCCTAGCTCTCCGACAGAAAGATGCGCTCTTTCGTGTGGAACCCAGATCA 839
 DB 61 TGCCTAGCTCTCCGACAGAAAGATGCGCTCTTTCGTGTGGAACCCAGATCA 120
 QY 840 GGAGGATTTGAGCCCGTGAAGAAATGAGAGAGATGGGGAACCTTGAACCTGAACGG 899
 DB 121 GGAGGATTTGAGCCCGTGAAGAAATGAGAGAGATGGGGAACCTTGAACCTGAACGG 180
 QY 900 GCAATTTGTTGTGCAACAACCGGTGAATGCCCAACCGTCCACAGAGATCAAGC 959
 DB 181 GCAATTTGTTGTGCAACAACCGGTGAATGCCCAACCGTCCACAGAGATCAAGC 240
 QY 960 AGCGGCTGGGAAGCCAGCAAAAGATGAGAGAGAGCTGACATGATCATCTGCAGAGCCT 1019
 DB 241 AGCGGCTGGGAAGCCAGCAAAAGATGAGAGAGAGCTGACATGATCATCTGCAGAGCCT 300
 QY 1020 GCTGACAGACTGCTGATGTTTGCAGCCCTGATGACAGAGCTTCTGCGGCTTGTACTC 1079
 DB 301 GCTGACAGACTGCTGATGTTTGCAGCCCTGATGACAGAGCTTCTGCGGCTTGTACTC 360
 QY 1080 GGGCTGATGAGGCGCTGCTCTGTGCTTACCTGCGGCTGCTCCGTTGAGCGGATCTG 1139
 DB 361 GGGCTGATGAGGCGCTGCTGTGCTGCTTACCTGCGGCTGCTCCGTTGAGCGGATCTG 420

RESULT 36
 CN428707 590 bp mRNA linear EST 16-MAY-2004
 LOCUS CN428707 17000600232773 GEN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION CN428707
 ACCESSION CN428707.1 GI:47416301
 VERSION CN428707.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 590)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 TITLE Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6): 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 1. 590
 Location/Qualifiers
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"

/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hes cell line H7"
/clone_id="GRN_PRENED"
/note="oligo dr primed, full-length enriched cDNA library
from hes cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 15.7%; Score 420; DB 7; Length 590;
Best Local Similarity 100.0%; Pred. No. 5.3e-198;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2242 TTATCCCTCTGAGTGAACCTCTCCAGAGCCCGGGGCGGAGCCCTCTGCTG 2301
DB 100 TTATCCCTCTGAGTGAACCTCTCCAGAGCCCGGGGCGGAGCCCTCTGCTG 159
QY 2302 AGCGCTGGGCGAGGCTCTGTGTGATCAGCAGAGAGAGAGAGAGAGAGAG 2361
DB 160 AGCGCTGGGCGAGGCTCTGTGTGATCAGCAGAGAGAGAGAGAGAGAGAG 219
QY 2362 GGCCTGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2421
DB 220 GGCCTGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 279
QY 2422 AGCAGAGTCTGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2481
DB 280 AGCAGAGTCTGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 339
QY 2482 GTTTCAG 2541
DB 340 GTTTCAG 399
QY 2542 GGGAG 2601
DB 400 GGGAG 459
QY 2602 TAAAGTTTAAATGTCAAACTGTAGCAAAATTAATTAATTAATTAATTA 2661
DB 460 TAAAGTTTAAATGTCAAACTGTAGCAAAATTAATTAATTAATTAATTA 519

RESULT 37

LOCUS BQ876252 876 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT 8681666 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376937
5', mRNA sequence.

ACCESSION BQ876252
VERSION BQ876252.1 GI:22268258
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: c9abbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.jnl.gov
Plate: L16M2559 row: 0 column: 18
High quality sequence stop: 678.
Location/Qualifiers

FEATURES

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/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:6376937"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_43"
/note="Organ: eye; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 15.7%; Score 420; DB 5; Length 876;
Best Local Similarity 99.5%; Pred. No. 5.3e-198;
Matches 660; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1165 GTGAGAGATACCTCATCAGATCCAGACAAAGTGCAGTGAAGATGTGCAAGT 1224
DB 1 GTGAGAGATACCTCATCAGATCCAGACAAAGTGCAGTGAAGATGTGCAAGT 60
QY 1225 ATGATGCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1284
DB 61 ATGATGCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
QY 1285 TCTGATGAAG 1344
DB 121 TCTGATGAAG 180
QY 1345 TCAGCATTAGACAGACATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1404
DB 181 TCAGCATTAGACAGACATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 1405 GCGAGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1464
DB 241 GCGAGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 1465 GATGACACCTCCAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1524
DB 301 GATGACACCTCCAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
QY 1525 CAAG 1584
DB 358 CAAG 417
QY 1585 GCGAG 1644
DB 418 GCGAG 477
QY 1645 CACCTGTACTGAGGAGCTGACACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1704
DB 478 CACCTGTACTGAGGAGCTGACACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
QY 1705 CTCAACCTGGGTGACAAAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1764
DB 538 CTCAACCTGGGTGACAAAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
QY 1765 ATCCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1824
DB 598 ATCCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 657
QY 1825 CTC 1827
DB 658 CTC 660

RESULT 38

LOCUS AW957709 650 bp mRNA linear EST 01-JUN-2000
DEFINITION EST369779 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW957709

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VERSION      AM957709.1  GI:8147392
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
              1 (bases 1 to 650)
              Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
              Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
              Quackenbush, J.
TITLE        Assessment of gene expression patterns in a model of colon tumor
              metastasis using a 15,200 element cDNA microarray
              Unpublished (2000)
JOURNAL      The Institute for Genomic Research
COMMENT      9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 3528
              Fax: 301 838 0208
              Email: johnq@tigr.org
              Plate: 110
              Seq primer: Reverse.
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Best Local Similarity 100.0%; Pred. No. 5.3e-197;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2242 TTTACCTCTGAGTGAAGACCTTCCCAAGACCCCGGGGCGGAGCCCTCTCTGCTG 2301
        |||||||
        158 TTTACCTCTGAGTGAAGACCTTCCCAAGACCCCGGGGCGGAGCCCTCTCTGCTG 217
QY      2302 AGCGCTGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2361
        |||||||
        218 AGCGCTGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 227
QY      2362 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2421
        |||||||
        278 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
QY      2422 AGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2481
        |||||||
        338 AGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2397
QY      2482 GTTTCAGAGAGGAGGAGCATAGTTACAGCCTTACAGAGAGGAGGAGGAGGAGG 2541
        |||||||
        398 GTTTCAGAGAGGAGGAGCATAGTTACAGCCTTACAGAGAGGAGGAGGAGGAGG 2457
QY      2542 GGGAAACACACAGCATTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2601
        |||||||
        458 GGGAAACACACAGCATTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 517
QY      2602 TTAGATTATTAATGTCACAACTGTCAGCAATATATATATATATATATATATATG 2659
        |||||||
        518 TTAGATTATTAATGTCACAACTGTCAGCAATATATATATATATATATATATATG 575
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Db

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REFERENCE    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS      1 (bases 1 to 414)
              Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flak, G. J.,
              Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
              Lebikowski, J. and Stanton, L. W.
TITLE        Transcriptional characterization elucidates signaling networks that
              control human ES cell growth and differentiation
JOURNAL      Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT      Contact: Brandenberger R
              Regenerative Medicine
              Genon Corporation
              230 Constitution Drive, Menlo Park, CA 94025, USA
              Tel: 650 473 8658
              Fax: 650 473 7760
              Email: rbrandenberger@genon.com
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              H9"
              /clone_1lb="GRN ES"
              /note="oligo dt primed, full-length enriched cDNA library
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              and H9 (p26) maintained in feeder-free conditions"
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Best Local Similarity 100.0%; Pred. No. 5.3e-195;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      54 GTTCCGGGTTGGGCGCGGGCGGGGATGTAATCCGATGAGCGGCGCGAGAGGCGAA 113
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        1 GTTCCGGGTTGGGCGCGGGCGGGGATGTAATCCGATGAGCGGCGCGAGAGGCGAA 60
QY      114 GCAAGTGGCGCGCGCGAGCCCTGGGGGAGCGGCTCCGCTGCTGGGGCGGAGAGGCGCA 173
        |||||||
        61 GCAAGTGGCGCGCGCGAGCCCTGGGGGAGCGGCTCCGCTGCTGGGGCGGAGAGGCGCA 120
QY      174 GCCGACGTCCTCTGAGGAGCGGAGAGTGAACAATCGGCGGAGACGAGGTTGCGACCT 233
        |||||||
        121 GCCGACGTCCTCTGAGGAGCGGAGAGTGAACAATCGGCGGAGACGAGGTTGCGACCT 180
QY      234 TTCCTTCCCGACATTAACCTGCTCTGGAATCACTGTAAATTTGATGATGAAAA 293
        |||||||
        181 TTCCTTCCCGACATTAACCTGCTCTGGAATCACTGTAAATTTGATGATGAAAA 240
QY      294 ATCAGGTGAGTGAACCTGGAAGATACGACGACCGATGGAACAGGATTAACAAGCTGA 353
        |||||||
        241 ATCAGGTGAGTGAACCTGGAAGATACGACGACCGATGGAACAGGATTAACAAGCTGA 300
QY      354 GGTGTTAAGAGACAGACATGCTTTACAGACTGGGAGATGTCATCTAGTGTGACAG 413
        |||||||
        301 GGTGTTAAGAGACAGACATGCTTTACAGACTGGGAGATGTCATCTAGTGTGACAG 360
QY      414 GAAAGATGAACCGGAACACACAGCTGCGCATCTCTATGATCTTTTAAGTGAAGA 467
        |||||||
        361 GAAAGATGAACCGGAACACACAGCTGCGCATCTCTATGATCTTTTAAGTGAAGA 414
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Db

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RESULT 39
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DEFINITION 17000532786421 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN428708
VERSION     CN428708.1  GI:47416302
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Euteleostomi;
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RESULT 40
LOCUS       CN428710      614 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 17000455366473 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN428710
VERSION     CN428710.1  GI:47416304
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Euteleostomi;
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE 1 (baes 1 to 614)
 AUTHORS Brandenberger R., Wei H., Zhang S., Lei S., Murage J., Fisk G.J.,
 Li Y., Xu C., Fang R., Guebler K., Rao M.S., Mandlam R.,
 Lebkowski J. and Stanton L.W.
 TITLE Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 /db_xref="taxon:9606"
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 H9"
 /clone_jib="GRN BS"
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 and H9 (p26) maintained in feeder-free conditions"
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 Best Local Similarity 100.0%; Pred. No. 5,3e-194; Indels 0; Gaps 0;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 GAATCCGATGAGCGGCCCGAGAGAGCGACAGTCCGCCGCCGACCCCTGGGAC 142
 DB 39 GAATCCGATGAGCGGCCCGAGAGAGCGACAGTCCGCCGCCGACCCCTGGGAC 98
 QY 143 GGCCTCTCGCTCTGGCCCGAGAGAGGGCGAGCGCAGTCCCTCTAGAGAAAGCGGAGT 202
 DB 99 GGCCTCTCGCTCTGGCCCGAGAGAGGGCGAGCGCAGTCCCTCTAGAGAAAGCGGAGT 158
 QY 203 GGACCATGGGCGAGAGAGAGGTTCCGACCTTCCCTCCCGACAAATTAAGTCTCTG 262
 DB 159 GGACCATGGGCGAGAGAGAGGTTCCGACCTTCCCTCCCGACAAATTAAGTCTCTG 218
 QY 263 GAGATCACTGTGAATTTGTATGTGATGAAAAATCAAGTCAAGTGAACCTGGAATTAACA 322
 DB 219 GAGATCACTGTGAATTTGTATGTGATGAAAAATCAAGTCAAGTGAACCTGGAATTAACA 278
 QY 323 GCACCAAGTGAACAGTGAATTAACAAGCTGAAGTGTGTTAAGAGAGACATGCCCTTAC 382
 DB 279 GCACCAAGTGAACAGTGAATTAACAAGCTGAAGTGTGTTAAGAGAGACATGCCCTTAC 338
 QY 383 AGACTGGGAGTGTCACTTCACTTGTGTGTCAGGAAGATGAACCGGAACAACGTTGCAT 442
 DB 339 AGACTGGGAGTGTCACTTCACTTGTGTGTCAGGAAGATGAACCGGAACAACGTTGCAT 398
 QY 443 ACCCTATGAATCTTAAGTGAAGAAAGCAAGGATGACCAAGATCCTTTGA 494
 DB 399 ACCCTATGAATCTTAAGTGAAGAAAGCAAGGATGACCAAGATCCTTTGA 450
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 DEFINITION 602328653F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4650348 5',
 mRNA sequence.
 ACCESSION BG481936
 VERSION BG481936.1 GI:13414215
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE	1 (bases 1 to 635)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Straubeberg, Ph.D. Email: cgads-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://Image.lnl.gov Plate: LNCM431 row: j column: 13 High quality sequence stop: 635. Location/Qualifiers
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ORIGIN	
Query Match	15.4%; Score 412; DB 4; Length 635;
Best Local Similarity	100.0%; Pred. No. 5.3e-194;
Matches	412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	83 GAATCCCGATGAGACGGCCCGAGAGACGATGCGCGCCGACGCTTGGGAC 142
Db	2 GAATCCCGATGAGACGGCCCGAGAGACGATGCGCGCCGACGCTTGGGAC 61
Qy	143 GGCTCTGCGCTGCGGCGGAGAGGCGGACGCGACGTCCTCTGAGAAAGCGGAGT 202
Db	62 GGCTCTGCGCTGCGGCGGAGAGGCGGACGCGACGTCCTCTGAGAAAGCGGAGT 121
Qy	203 GGACCATCGGCGGAGACGAGGTTGCGACCTTTCTTCCCGACGATTAACCTGCTCTG 262
Db	122 GGACCATCGGCGGAGACGAGGTTGCGACCTTTCTTCCCGACGATTAACCTGCTCTG 181
Qy	263 GAGATCACTGAGAAATGTGTGTGATGTAATAAATCAGGTCAGGTGACACTGGAAGTACCA 322
Db	182 GAGATCACTGAGAAATGTGTGTGATGTAATAAATCAGGTGACACTGGAAGTACCA 241
Qy	323 GCACCAAGTGAACAGTATTAACAAGTGAAGGTTGTTAAGAACAGACATGCTTTTAC 382
Db	242 GCACCAAGTGAACAGTATTAACAAGTGAAGGTTGTTAAGAACAGACATGCTTTTAC 301
Qy	383 AGACTGGGAGATGTCATCTAATTGTTGTAACAGAAATGAACCGGAACACACGCGAT 442
Db	302 AGACTGGGAGATGTCATCTAATTGTTGTAACAGAAATGAACCGGAACACACGCGAT 361
Qy	443 ACCTCTATGATCTTTAAGTGAAGAAAGGACATGACACAGAATCCTTTGA 494
Db	362 ACCTCTATGATCTTTAAGTGAAGAAAGGACATGACACAGAATCCTTTGA 413
RESULT 42	
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LOCUS	BF109790
DEFINITION	7169a04.x1 Soares_NSF_P8_9M_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3526543 3', mRNA sequence.	
ACCESSION	BF109790

VERSION BF109790.1 GI:10939480
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 490)
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from Glibco
 High quality sequence stop: 460.
 Location/Qualifiers
 1..490
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3526543"
 /lab_host="DH10B"
 /note="Soares NSF, 9W OT PA P S1"
 /note="Organ: pooled; Vector: pFRTD-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI.
 Equal amounts of plasmid DNA from five normalized libraries were mixed, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHR pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOF pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and W. Fatima Bernaldo."

ORIGIN

Query Match 15.3%; Score 409; DB 2; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.7e-192; Indels 0; Gaps 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2251 TGAAGTGAACCTCCAGAGCCCGGAGCCCGCTCTGCTGAGCGCTGG 2310
 409 TGAAGTGAACCTCCAGAGCCCGGAGCCCGCTCTGCTGAGCGCTGG 350
 2311 CAGGGCTCGTGTGATCAGCAGAGAGAGAGCTTCTGTAACATGCGGCGTCCC 2370
 349 CAGGGCTCGTGTGATCAGCAGAGAGAGAGCTTCTGTAACATGCGGCGTCCC 290
 2371 GCGGAGAGGGGAGCTTGTCTCTTGTGATCTTCCGAACTACAGTTAAACCAAGT 2430
 289 GCGGAGAGGGGAGCTTGTCTCTTGTGATCTTCCGAACTACAGTTAAACCAAGT 230
 2431 CTGTTTTCAGAAAAGTTTCAAGGAGAGAGCAAGTTTATCAAAACATTTGTTTCA 2490
 229 CTGTTTTCAGAAAAGTTTCAAGGAGAGAGCAAGTTTATCAAAACATTTGTTTCA 170
 2491 GAAAGGAGCATTAAGTTTACAGCTTACAGAGAGAGAGCAATATCTCTGCTGGGAAAAC 2550
 169 GAAAGGAGCATTAAGTTTACAGCTTACAGAGAGAGAGCAATATCTCTGCTGGGAAAAC 110
 2551 ACAGCATTTATATTTTATTTTAAATAGTTGCTATCTCTTAAATAGTTTAA 2610
 109 ACAGCATTTATATTTTATTTTAAATAGTTGCTATCTCTTAAATAGTTTAA 50
 2611 AATGTCAAACTGTAGACAAATATATATTTTAAATTTTCAAAATG 2659

Db 49 AATGTCAAACTGTAGACAAATATATATTTTAAATTTTCAAAATG 1

RESULT 43
 LOCUS BU153737
 DEFINITION BU153737
 AGENCOURT 7889369 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6142354
 5', mRNA sequence.
 ACCESSION BU153737
 VERSION BU153737.1 GI:22667269
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 881)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: L1AM13464 row: a column: 11
 High quality sequence stop: 621.
 Location/Qualifiers
 1..881
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6142354"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

FEATURES

source

ORIGIN

Query Match 15.1%; Score 404; DB 5; Length 881;
 Best Local Similarity 100.0%; Pred. No. 5.3e-190; Indels 0; Gaps 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 30 TTGACAGCGCGCGCGCGAGCGGTTCCGGGTTGCGCGCGGAGATGGAATCCC 89
 1 TTGACAGCGCGCGCGCGAGCGGTTCCGGGTTGCGCGCGGAGATGGAATCCC 60
 90 GATGAGCGCGCGCGAG 149
 61 GATGAGCGCGCGCGAG 120
 150 GCGTCTGGGCGCGAT 209
 121 GCGTCTGGGCGCGAT 180
 210 CCGGCGGAT 269
 181 CCGGCGGAT 240
 270 CTGTGAATTTAGTGAAGAAATACAGTACAGTGAACCTGAAGATACAGACAG 329
 241 CTGTGAATTTAGTGAAGAAATACAGTACAGTGAACCTGAAGATACAGACAG 300
 330 TGGAACTGATTAACAAGCTGAAGGTTTAAAGAGAGAGAGAGAGAGAGAGAGAG 389
 301 TGGAACTGATTAACAAGCTGAAGGTTTAAAGAGAGAGAGAGAGAGAGAGAGAG 360

QY 390 GGATGTCATCTACTTGTTGTAACAGAGATGATGACCGAACA 433
 DB 361 GAGTTCATCTACTTGTTGTAACAGAGATGATGACCGAACA 404

RESULT 44
 LOCUS BX409790 940 bp mRNA linear EST 01-MAY-2004
 DEFINITION BX409790 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DP017Y11.9 5-PRIME, mRNA sequence.

ACCESSION BX409790
 VERSION BX409790.2 GI:46933826
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS L.W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 13, 2003 this sequence version replaced gi:30656944.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st enriched cDNA was primed with a NotI-oligo (dr) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6792.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0BAF0142C07_AFO1300_1&c=6792.r

FEATURES

source 1. 940
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DP017Y11.9"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_1lb="Homo sapiens FETAL BRAIN"
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo (dr) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 14.7%; Score 394; DB 5; Length 940;
 Best Local Similarity 100.0%; Pred. No. 5.3e-185;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1772 AGAATTAAGTCTGCAACCAAGGTTTGAATGAAAAAATGTTGACCGAGACCTTCGTG 1831
 DB 199 AGAATTAAGTCTGCAACCAAGGTTTGAATGAAAAAATGTTGACCGAGACCTTCGTG 258
 QY 1832 CTCTCAGGCGGGAAGTGTCTGCTGTGATTAAGAGTCAACGAGGAGACACCGTTCTGT 1891
 DB 259 CTCTCAGGCGGGAAGTGTCTGCTGTGATTAAGAGTCAACGAGGAGACACCGTTCTGT 318
 QY 1892 GTTACTGCTGTGAGCTGCGCAGCTTCGTTGAGCTGAACCTATGATTCGCGAACAATTC 1951
 DB 319 GTTACTGCTGTGAGCTGCGCAGCTTCGTTGAGCTGAACCTATGATTCGCGAACAATTC 378
 QY 1952 CTGCTTCGAGATTGCGAGTGGCGGTAACTCCGTTCTGATGCTAATCTGGGGCCGTAATC 2011
 DB 379 CTGCTTCGAGATTGCGAGTGGCGGTAACTCCGTTCTGATGCTAATCTGGGGCCGTAATC 438
 QY 2012 GCGGCACTGAGGTGAAGCTCAACGAGCATGAAATTCATCATCTGTGAACAGACA 2071

DB 439 GCGGCACTGAGGTGAAGCTCAACGAGCATGAAATTCATCATCTGTGAACAGACA 498
 QY 2072 GGTTCAAAACTAAGCATTCAGAGGCTTGAAGCAGCTTTACAGCACTGAGTGAAGAG 2131
 DB 499 GGTTCAAAACTAAGCATTCAGAGGCTTGAAGCAGCTTTACAGCACTGAGTGAAGAG 558

RESULT 45
 LOCUS AI200393 475 bp mRNA linear EST 14-OCT-1998
 DEFINITION AI200393.1 Scaree_fetal_lung_MbH19w Homo sapiens cDNA clone
 IMAGE:1756926 3', mRNA sequence.

ACCESSION AI200393
 VERSION AI200393.1 GI:3752999
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -40UP from Glenco
 High quality sequence stop: 474.

FEATURES

source 1. 475
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1756926"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_1lb="Scaree fetal lung MbH19w"
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo (dr) primer
 [5'-TGTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Benito
 Soares and M. Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart MbH19w."

ORIGIN

Query Match 14.4%; Score 386; DB 1; Length 475;
 Best Local Similarity 100.0%; Pred. No. 5.3e-181;
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2276 GGGGGCCGACCGCCCTCTCTGTGAGACGTTGGGAGAGGCTTCGTGCGATCAGCAGC 2335
 DB 474 GGGGGCCGACCGCCCTCTCTGTGAGACGTTGGGAGAGGCTTCGTGCGATCAGCAGC 415
 QY 2336 AGAGCAAGGCTTCTGTACATGCGGCGTCCGCGAGAGGGGAGTTTGTCTTTT 2395
 DB 414 AGAGCAAGGCTTCTGTACATGCGGCGTCCGCGAGAGGGGAGTTTGTCTTTT 355
 QY 2396 TGTACATTTTCGAAATCTAGATTAAAGCAGAGTCTGTTTCAGAAAAGTTTCAAGGG 2455
 DB 354 TGTACATTTTCGAAATCTAGATTAAAGCAGAGTCTGTTTCAGAAAAGTTTCAAGGG 295

QY 2456 AGAAGGCAAGTTTCAAAAACATTTCTCAGAGAGGAGCATTAAGTTTACAGCCTA 2515
 DB 294 AGAAGGCAAGTTTCAAAAACATTTCTCAGAGAGGAGCATTAAGTTTACAGCCTA 235
 QY 2516 CAGAGAGTACACATATCTCTGCTGGGAAAACACAGATTTTATCTATTTTATTT 2575
 DB 234 CAGAGAGTACACATATCTCTGCTGGGAAAACACAGATTTTATCTATTTTATTT 175
 QY 2576 TAATAGTTTGGTCTATCTCTGAATTAATTAATGTCACAACTGTAGACAAAT 2635
 DB 174 TAATAGTTTGGTCTATCTCTGAATTAATTAATGTCACAACTGTAGACAAAT 115
 QY 2636 ATATAATTTATTAATTAACAATTAATGAC 2661
 DB 114 ATATAATTTATTAATTAACAATTAATGAC 89

RESULT 46
 CN481126 618 bp mRNA linear EST 26-APR-2004
 LOCUS hw03c10.y1 Human primary human ocular pericytes. Unamplified (hw)
 DEFINITION Homo sapiens cDNA clone hw03c10.5', mRNA sequence.
 ACCESSION CN481126
 VERSION CN481126.1 GI:46562630
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Tsai, J.Y. and Wistow, G.
 1 (bases 1 to 618)
 Tsal, J.Y. and Wistow, G.
 Expressed sequence tag analysis of cultured primary human ocular
 pericytes
 JOURNAL Unpublished (2004)
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: gwaem@helix.nih.gov
 Plate: 03 row: C column: 10
 Seg primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers
 1..618
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="hw03c10"
 /cell_type="pericytes"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human primary human ocular pericytes."
 /note="Organ: Eye; Vector: pSPORT1; RNA was extracted from
 primary human pericytes in culture. A directionally cloned
 cDNA library in the pSPORT1 vector (Invitrogen) was
 essentially following the protocols of the Superscript
 Plasmid System full details of which are contained in the
 manufacturer's instruction manual
 (http://www.lifetech.com/). First strand synthesis was
 carried out using a Not I primer-adaptor
 (5'-GACAGTCTGATCGGAGCGGCCCTT)15-3'. cDNA was
 cloned in Not I/Sal I sites. EST analysis was performed at
 the NIH Intramural Sequencing Center (NISC)."

ORIGIN
 Query Match 14.4%; Score 386; DB 7; Length 618;
 Best Local Similarity 99.8%; Pred. No. 5.3e-181;
 Matches 436; Conservative 0; Mismatch 1; Indels 0; Gaps 0;

QY 1806 AAACATGTTGACGAGAGGCTGTGCTCTCCAGCGGAGAGTGTCTGTCTGATTA 1865

DB 115 AAACATGTTGACGAGAGGCTGTGCTCTCCAGCGGAGAGTGTCTGTCTGATTA 174
 QY 1866 CAGAGTACGAGGAGACACCGTTCTGTGTTATCTGTGACCTGCGAGCTTCCGTAAGT 1925
 DB 175 CAGAGTACGAGGAGACACCGTTCTGTGTTATCTGTGACCTGCGAGCTTCCGTAAGT 234
 QY 1926 GACCTATCAGTATCGGACAGAACTTCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCG 1985
 DB 235 GACCTATCAGTATCGGACAGAACTTCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCG 294
 QY 1986 TCTGACCTGCTACTGAGGAGCGTAACTGCGGACTGAGTGAAGCTCACACGCCATGAA 2045
 DB 295 TCTGACCTGCTACTGAGGAGCGTAACTGCGGACTGAGTGAAGCTCACACGCCATGAA 354
 QY 2046 ATTCAATCATATCTGTGAAACAGACAGGTTCAAAAACCTAAGCATTCAGAGGCCCTGAGCA 2105
 DB 355 ATTCAATCATATCTGTGAAACAGACAGGTTCAAAAACCTAAGCATTCAGAGGCCCTGAGCA 414
 QY 2106 GCTTTCAGACTGAGGAGTGAAGAGCGCTTTTAAATTAACAGACAAAGCATGCAAG 2165
 DB 415 GCTTTCAGACTGAGGAGTGAAGAGCGCTTTTAAATTAACAGACAAAGCATGCAAG 474
 QY 2166 GTGTTTTCACAGCCCCCTGAGGAGGAGGACGACAGGCTCTCCGACAGTGTCTGAGGTGA 2225
 DB 475 GTGTTTTCACAGCCCCCTGAGGAGGAGGACGACAGGCTCTCCGACAGTGTCTGAGGTGA 534
 QY 2226 CTCTTCTGTGAGCTTT 2242
 DB 535 CTCTTCTGTGAGCTTT 551

RESULT 47
 BG831289 824 bp mRNA linear EST 22-MAY-2001
 LOCUS 602766120P1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:490816.5',
 DEFINITION mRNA sequence.
 ACCESSION BG831289
 VERSION BG831289.1 GI:14178876
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 824)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM1814 row: G column: 05
 High quality sequence stop: 745.
 Location/Qualifiers
 1..824
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:490816"
 /tissue="IMR90:epithelial carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_42"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling

ORIGIN

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

Query Match 14.3%; Score 382; DB 4; Length 824;
Best Local Similarity 99.8%; Pred. No. 5.3e-179;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1810 ATGTGACCGAGAGCGCTGCTCCAGCGGGAGTGTTCGTGCTGATTAACGA 1869
DB 2 ATGTGACCGAGAGCGCTGCTCCAGCGGGAGTGTTCGTGCTGATTAACGA 61
QY 1870 GTACGGGAGACACCGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929
DB 62 GTACGGGAGACACCGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121

QY 1930 TATCATATCGGACAACTTCCTGCTCCAGTTCGAGTCCGCTGATTCCTGCT 1989
DB 122 TATCATATCGGACAACTTCCTGCTCCAGTTCGAGTCCGCTGATTCCTGCT 181

QY 1990 GACTGCTACTGGGGCCGTAACTGCGCACTCAGGTGAAGCTCACCAGCGCATGAATTC 2049
DB 182 GACTGCTACTGGGGCCGTAACTGCGCACTCAGGTGAAGCTCACCAGCGCATGAATTC 241

QY 2050 AATCATATCTGTGAACAGCAAGGTTCAAAACTAAGCATCCAGGCGCTGAGAGCTT 2109
DB 242 AATCATATCTGTGAACAGCAAGGTTCAAAACTAAGCATCCAGGCGCTGAGAGCTT 301

QY 2110 TCAGCACTGAGAGTGAAGAGCGCTGTTTAAATACAGACAAACGCTCAAGGTCT 2169
DB 302 TCAGCACTGAGAGTGAAGAGCGCTGTTTAAATACAGACAAACGCTCAAGGTCT 361

QY 2170 TTTCACAGCGCCCTGAGGAGGAGGAGGCTCTCCAGAGTGTCTGAGGTGACTT 2229
DB 362 TTTCACAGCGCCCTGAGGAGGAGGAGGCTCTCCAGAGTGTCTGAGGTGACTT 421

QY 2230 TCTGTGAGCTTT 2242
DB 422 TCTGTGAGCTTT 434

RESULT 48
BI460002 797 bp mRNA linear EST 21-AUG-2001
LOCUS 603201532F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267575 5',
DEFINITION mRNA sequence.
ACCESSION BI460002
VERSION BI460002.1 GI:15250658
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1674 row: P column: 08
High quality sequence stop: 793.
Location/Qualifiers
1. 797

FEATURES
SOURCE

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5267575"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTT-3', size-selected for average
insert size 2.2 kb and normalized to R0.5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

Query Match 14.2%; Score 381; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 1.7e-178;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGTTCGGGTTCCGGCGGGGCGGAGTGAATCCGATGAGCGGCCGAGAGAGCA 112
DB 9 GGTTCGGGTTCCGGCGGGGCGGAGTGAATCCGATGAGCGGCCGAGAGAGCA 68

QY 113 AGCAGTCGCGCGCGCGCGAGCTTGGGAGCGCTCTGCTGCGCGCGAGAGAGGCG 172
DB 69 AGCAGTCGCGCGCGCGCGAGCTTGGGAGCGCTCTGCTGCGCGCGAGAGAGGCG 128

QY 173 AGCGGAGTCTCTCTGAGAGAGGAGAGTGAACATCGGGCGGAGAGAGGCTT 232
DB 129 AGCGGAGTCTCTCTGAGAGAGGAGAGTGAACATCGGGCGGAGAGAGGCTT 188

QY 223 TTTCTTCCCGAGCAATTAATCTGCTCTGAGATCACTGATTAATTGATGATGAAA 292
DB 189 TTTCTTCCCGAGCAATTAATCTGCTCTGAGATCACTGATTAATTGATGATGAAA 248

QY 293 AATCAGTCACTGACACTGGAAGATACAGACACAGTGAACAGTGAACAAGCTGA 352
DB 249 AATCAGTCACTGACACTGGAAGATACAGACACAGTGAACAGTGAACAAGCTGA 308

QY 353 AGTTGTTAAAGACAGACATGCTTAAAGACTGAGGAGATGATCACTGATGATCA 412
DB 309 AGTTGTTAAAGACAGACATGCTTAAAGACTGAGGAGATGATCACTGATGATCA 368

QY 413 GGAAGATGAACCGGACACA 433
DB 369 GGAAGATGAACCGGACACA 389

RESULT 49
BM802324 1070 bp mRNA linear EST 05-MAR-2002
LOCUS BM802324
DEFINITION AGENCOURT_6460403 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:555833
5', mRNA sequence.
ACCESSION BM802324
VERSION BM802324.1 GI:19119147
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

FEATURES
SOURCE

101	21	0.8	915	3	US-09-724-864-14	Sequence 14, Appl	C 174	20	0.7	63	4	US-09-270-767-26835	Sequence 26835, A
C 102	21	0.8	916	4	US-09-270-767-3380	Sequence 3380, Ap	C 175	20	0.7	70	2	US-08-776-944-12	Sequence 12, Appl
C 103	21	0.8	916	4	US-09-270-767-18662	Sequence 18662, A	C 176	20	0.7	75	4	US-09-621-976-15078	Sequence 15078, A
104	21	0.8	935	1	US-08-313-050-10	Sequence 10, Appl	177	20	0.7	76	3	US-09-244-794A-1	Sequence 1, Appl1
105	21	0.8	993	3	US-08-924-747-17	Sequence 17, Appl	178	20	0.7	76	3	US-09-247-190-1	Sequence 1, Appl1
106	21	0.8	993	3	US-09-247-373B-17	Sequence 17, Appl	179	20	0.7	76	4	US-09-238-710-1	Sequence 1, Appl1
107	21	0.8	993	3	US-09-296-715-17	Sequence 17, Appl	180	20	0.7	78	4	US-09-513-999C-18461	Sequence 18461, A
108	21	0.8	1020	3	US-09-201-641-17	Sequence 17, Appl	181	20	0.7	81	4	US-09-270-767-4681	Sequence 4681, Ap
109	21	0.8	1088	4	US-09-489-847-80	Sequence 80, Appl	182	20	0.7	81	4	US-09-270-767-19963	Sequence 19963, A
110	21	0.8	1177	4	US-09-799-451-73	Sequence 73, Appl	183	20	0.7	87	4	US-09-621-976-14849	Sequence 14849, A
111	21	0.8	1282	3	US-09-316A-69	Sequence 69, Appl	184	20	0.7	89	4	US-09-621-976-7745	Sequence 7745, Ap
112	21	0.8	1282	3	US-09-704-640-69	Sequence 69, Appl	C 185	20	0.7	90	3	US-09-065-058-16	Sequence 16, Appl
113	21	0.8	1301	4	US-09-489-847-108	Sequence 108, App	186	20	0.7	91	4	US-09-513-999C-30264	Sequence 30264, A
114	21	0.8	1315	3	US-08-908-332-3	Sequence 3, Appl1	187	20	0.7	92	4	US-09-621-976-13620	Sequence 13620, A
115	21	0.8	1318	5	PCT-US94-07127A-1	Sequence 5, Appl1	188	20	0.7	101	4	US-09-621-976-7753	Sequence 7753, Ap
116	21	0.8	1341	5	US-09-504-445-5	Sequence 5, Appl1	189	20	0.7	101	4	US-09-621-976-7778	Sequence 7778, Ap
117	21	0.8	1487	3	US-09-291-922-13	Sequence 13, Appl	190	20	0.7	101	4	US-09-621-976-7787	Sequence 7787, Ap
118	21	0.8	1624	4	US-09-647-224A-13	Sequence 13, Appl	191	20	0.7	101	4	US-09-621-976-19288	Sequence 19288, A
119	21	0.8	1626	4	US-09-743-207-7	Sequence 7, Appl	192	20	0.7	101	4	US-09-621-976-19290	Sequence 19290, A
120	21	0.8	1654	3	US-09-347-798-9	Sequence 9, Appl	193	20	0.7	101	4	US-09-621-976-19315	Sequence 19315, A
121	21	0.8	1557	3	US-08-094-071-1	Sequence 1, Appl1	194	20	0.7	101	4	US-09-621-976-19331	Sequence 19331, A
122	21	0.8	1577	5	PCT-US92-00878-1	Sequence 9, Appl1	195	20	0.7	111	3	US-08-991-789A-83	Sequence 83, Appl
123	21	0.8	1760	4	US-09-849-602-9	Sequence 9, Appl1	196	20	0.7	111	3	US-08-991-789A-145	Sequence 145, App
124	21	0.8	1953	3	US-08-826-246-1	Sequence 1, Appl1	197	20	0.7	111	3	US-09-062-451-83	Sequence 83, Appl
125	21	0.8	1953	3	US-08-944-495-1	Sequence 1, Appl1	198	20	0.7	111	3	US-09-062-451-145	Sequence 145, App
126	21	0.8	1953	3	US-09-126-640-1	Sequence 1, Appl1	199	20	0.7	111	4	US-09-598-326-83	Sequence 83, Appl
127	21	0.8	1953	3	US-08-925-588-1	Sequence 1, Appl1	200	20	0.7	111	4	US-09-598-326-145	Sequence 145, App
128	21	0.8	1953	3	US-09-828-292A-1	Sequence 1, Appl1	201	20	0.7	111	4	US-09-289-188-83	Sequence 83, Appl
129	21	0.8	1953	4	US-09-372-044-1	Sequence 1, Appl1	202	20	0.7	111	4	US-09-289-198-145	Sequence 83, App
130	21	0.8	1953	4	US-08-825-486-1	Sequence 1, Appl1	203	20	0.7	111	4	US-09-429-755-83	Sequence 83, Appl
131	21	0.8	1953	4	US-08-825-486-1	Sequence 1, Appl1	204	20	0.7	111	4	US-09-429-755-145	Sequence 145, App
132	21	0.8	2043	4	US-09-615-192A-266	Sequence 266, App	205	20	0.7	114	4	US-09-270-767-24312	Sequence 24312, A
133	21	0.8	2056	2	US-08-836-421-1	Sequence 1, Appl1	206	20	0.7	114	4	US-09-621-976-12903	Sequence 12903, A
134	21	0.8	2138	3	US-08-776-271-1	Sequence 1, Appl1	207	20	0.7	124	4	US-09-621-976-17503	Sequence 17503, A
135	21	0.8	2143	3	US-09-215-035-1	Sequence 13, Appl	208	20	0.7	127	4	US-09-621-976-13933	Sequence 13933, A
136	21	0.8	2383	2	US-08-274-318-1	Sequence 1, Appl	209	20	0.7	131	4	US-09-270-767-25268	Sequence 25268, A
137	21	0.8	2406	2	US-08-463-081B-1	Sequence 1, Appl1	210	20	0.7	134	4	US-09-270-767-26454	Sequence 26454, A
138	21	0.8	2406	2	US-08-461-379A-1	Sequence 1, Appl1	211	20	0.7	137	4	US-09-621-976-17502	Sequence 17502, A
139	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	212	20	0.7	150	4	US-09-621-976-13989	Sequence 13989, A
140	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	213	20	0.7	150	4	US-09-270-767-29737	Sequence 29737, A
141	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	214	20	0.7	154	4	US-09-513-999C-18252	Sequence 18252, A
142	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	215	20	0.7	165	4	US-09-621-976-15270	Sequence 15270, A
143	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	216	20	0.7	169	4	US-09-621-976-15270	Sequence 15270, A
144	21	0.8	2406	2	US-08-463-390B-1	Sequence 1, Appl1	C 217	20	0.7	170	4	US-09-270-767-25276	Sequence 25276, A
145	21	0.8	2432	4	US-09-205-258-48	Sequence 48, Appl	C 218	20	0.7	170	4	US-09-270-767-24553	Sequence 24553, A
C 146	21	0.8	2818	4	US-09-620-312D-92	Sequence 92, Appl	219	20	0.7	175	4	US-09-621-976-12172	Sequence 12172, A
C 147	21	0.8	2997	4	US-09-852-991A-11853	Sequence 11853, A	220	20	0.7	175	4	US-09-621-976-12883	Sequence 12883, A
148	21	0.8	3295	4	US-10-101-464A-463	Sequence 463, App	221	20	0.7	177	4	US-09-621-976-12662	Sequence 12662, A
149	21	0.8	3572	2	US-08-713-815A-2	Sequence 2, Appl1	222	20	0.7	179	4	US-09-621-976-15270	Sequence 15270, A
150	21	0.8	7286	3	US-09-331-581-3	Sequence 3, Appl1	223	20	0.7	180	4	US-09-621-976-15270	Sequence 15270, A
151	21	0.8	7705	2	US-08-687-080-115	Sequence 115, App	224	20	0.7	181	4	US-09-270-767-25769	Sequence 25769, A
152	21	0.8	7938	3	US-09-331-581-14	Sequence 14, Appl	225	20	0.7	184	4	US-09-270-767-3527	Sequence 3527, Ap
C 153	21	0.8	9299	3	US-08-458-434A-7	Sequence 7, Appl	226	20	0.7	184	4	US-09-270-767-18809	Sequence 18809, A
154	21	0.8	29604	3	US-08-781-891-207	Sequence 207, App	227	20	0.7	192	4	US-09-513-999C-16224	Sequence 16224, A
155	21	0.8	29604	4	US-09-618-166-207	Sequence 207, App	228	20	0.7	197	4	US-09-621-976-14874	Sequence 14874, A
156	21	0.8	107820	4	US-09-792-616-1	Sequence 1, Appl1	229	20	0.7	200	4	US-09-621-976-16166	Sequence 16166, A
157	20	0.7	25	1	US-08-113-646A-42	Sequence 42, Appl	230	20	0.7	201	4	US-09-621-976-11824	Sequence 11824, A
158	20	0.7	30	1	US-08-455-627-12	Sequence 12, Appl	231	20	0.7	201	4	US-09-621-976-11931	Sequence 11931, A
159	20	0.7	30	2	US-08-689-856-12	Sequence 12, Appl	232	20	0.7	201	4	US-09-621-976-11938	Sequence 11938, A
C 160	20	0.7	30	3	US-08-787-321-12	Sequence 12, Appl	233	20	0.7	201	4	US-09-621-976-11979	Sequence 11979, A
C 161	20	0.7	38	4	US-09-325-554-8	Sequence 8, Appl1	234	20	0.7	201	4	US-09-621-976-12109	Sequence 12109, A
C 162	20	0.7	38	4	US-09-325-554-8	Sequence 8, Appl1	235	20	0.7	201	4	US-09-621-976-15268	Sequence 15268, A
C 163	20	0.7	38	4	US-09-325-554-9	Sequence 9, Appl1	236	20	0.7	201	4	US-09-621-976-15269	Sequence 15269, A
C 164	20	0.7	38	4	US-10-102-720-8	Sequence 8, Appl1	237	20	0.7	201	4	US-09-621-976-15269	Sequence 15269, A
C 165	20	0.7	40	3	US-08-970-166-18	Sequence 18, Appl	238	20	0.7	201	4	US-09-621-976-16161	Sequence 16161, A
C 166	20	0.7	45	4	US-09-025-639-1	Sequence 1, Appl1	239	20	0.7	201	4	US-09-621-976-16163	Sequence 16163, A
C 167	20	0.7	45	4	US-09-333-237-1	Sequence 1, Appl1	240	20	0.7	201	4	US-09-621-976-16165	Sequence 16165, A
C 168	20	0.7	45	4	US-10-043-415-1	Sequence 1, Appl1	241	20	0.7	202	4	US-09-621-976-16167	Sequence 16167, A
C 169	20	0.7	55	4	US-09-513-999C-23966	Sequence 23966, A	242	20	0.7	202	4	US-09-621-976-16167	Sequence 16167, A
C 170	20	0.7	56	1	US-08-275-169-1	Sequence 1, Appl1	243	20	0.7	205	4	US-09-553-630-4	Sequence 630-4, A
C 171	20	0.7	60	4	US-09-410-960-1	Sequence 1, Appl1	244	20	0.7	211	4	US-09-270-767-2950	Sequence 2950, Ap
C 172	20	0.7	60	4	US-09-410-960-3	Sequence 3, Appl1	245	20	0.7	211	4	US-09-270-767-18232	Sequence 18232, A
C 173	20	0.7	60	4	US-09-410-960-4	Sequence 4, Appl1	246	20	0.7	212	4	US-09-621-976-1338	Sequence 1338, Ap

247	20	0.7	215	4	US-09-702-705-499	Sequence 499, App	320	20	0.7	397	4	US-09-270-767-13716	Sequence 13716, A
248	20	0.7	215	4	US-09-736-457-499	Sequence 499, App	321	20	0.7	401	4	US-09-270-767-13105	Sequence 13105, App
249	20	0.7	215	4	US-09-614-124B-499	Sequence 499, App	C 322	20	0.7	401	4	US-09-270-767-13458	Sequence 13458, A
250	20	0.7	215	4	US-09-671-325-499	Sequence 499, App	323	20	0.7	401	4	US-09-270-767-18387	Sequence 18387, App
251	20	0.7	215	4	US-09-589-184-499	Sequence 499, App	C 324	20	0.7	412	4	US-09-702-705-1047	Sequence 1047, App
252	20	0.7	215	4	US-09-658-824-499	Sequence 499, App	C 325	20	0.7	412	4	US-09-736-457-1047	Sequence 1047, App
253	20	0.7	223	4	US-09-621-976-11005	Sequence 11005, A	C 326	20	0.7	412	4	US-09-614-124B-1047	Sequence 1047, App
254	20	0.7	226	4	US-09-370-767-7669	Sequence 7669, App	C 327	20	0.7	412	4	US-09-671-325-1047	Sequence 1047, App
255	20	0.7	226	4	US-09-270-767-22951	Sequence 22951, A	C 328	20	0.7	412	4	US-09-658-824-1047	Sequence 1047, App
256	20	0.7	211	3	US-09-328-111-287	Sequence 287, App	329	20	0.7	425	4	US-09-621-976-15366	Sequence 15366, A
257	20	0.7	232	4	US-09-270-767-30766	Sequence 30766, A	330	20	0.7	426	4	US-09-621-976-15357	Sequence 15357, A
258	20	0.7	232	4	US-09-621-976-16632	Sequence 16632, A	C 331	20	0.7	432	3	US-09-470-473-7	Sequence 7, App1
259	20	0.7	241	4	US-09-389-681-334	Sequence 334, App	C 332	20	0.7	438	4	US-09-256-000-8	Sequence 8, App1
260	20	0.7	241	4	US-09-620-405B-334	Sequence 334, App	C 333	20	0.7	438	4	US-10-034-015A-8	Sequence 8, App1
261	20	0.7	241	4	US-09-433-826B-334	Sequence 334, App	C 334	20	0.7	443	4	US-09-270-767-9797	Sequence 9797, App
262	20	0.7	241	4	US-09-604-287A-334	Sequence 334, App	C 335	20	0.7	443	4	US-09-270-767-25069	Sequence 25069, A
263	20	0.7	241	4	US-09-834-759-334	Sequence 334, App	336	20	0.7	451	4	US-09-770-767-22429	Sequence 2429, App
264	20	0.7	250	4	US-09-590-751A-334	Sequence 13021, A	337	20	0.7	451	4	US-09-270-767-17711	Sequence 17711, A
265	20	0.7	250	4	US-09-621-976-13021	Sequence 13021, A	338	20	0.7	454	4	US-09-621-976-15365	Sequence 15365, A
266	20	0.7	258	4	US-09-621-976-11082	Sequence 11082, A	339	20	0.7	455	4	US-09-621-976-15365	Sequence 15365, A
267	20	0.7	259	4	US-09-621-976-14798	Sequence 14798, A	340	20	0.7	467	4	US-09-270-767-5956	Sequence 5956, App
268	20	0.7	260	4	US-09-270-767-31002	Sequence 31002, A	341	20	0.7	467	4	US-09-270-767-21238	Sequence 21238, A
269	20	0.7	260	4	US-09-621-976-13627	Sequence 13627, A	C 342	20	0.7	473	4	US-09-919-039-244	Sequence 244, App
270	20	0.7	269	4	US-09-270-767-9211	Sequence 9211, App	343	20	0.7	474	4	US-09-149-476-13	Sequence 13, App1
271	20	0.7	269	4	US-09-270-767-24493	Sequence 24493, A	344	20	0.7	474	4	US-09-621-976-1006	Sequence 1006, App
272	20	0.7	273	4	US-09-621-976-59	Sequence 59, App1	345	20	0.7	476	4	US-09-270-767-12396	Sequence 12396, A
273	20	0.7	275	4	US-09-270-767-2418	Sequence 2418, App	C 346	20	0.7	478	4	US-09-270-767-10173	Sequence 10173, A
274	20	0.7	275	4	US-09-270-767-17700	Sequence 17700, A	347	20	0.7	486	4	US-09-817-318-11	Sequence 11, App1
275	20	0.7	282	4	US-09-270-767-28156	Sequence 28156, A	348	20	0.7	490	4	US-09-854-133-685	Sequence 685, App
276	20	0.7	286	4	US-09-270-767-29002	Sequence 29002, A	349	20	0.7	492	3	US-08-946-026-43	Sequence 43, App1
277	20	0.7	287	4	US-09-621-976-17997	Sequence 17997, A	350	20	0.7	513	4	US-09-288-143-31	Sequence 31, App1
278	20	0.7	291	4	US-09-270-767-27027	Sequence 27027, A	351	20	0.7	519	4	US-09-270-767-4538	Sequence 4538, App
279	20	0.7	297	4	US-09-270-767-7863	Sequence 7863, App	352	20	0.7	519	4	US-09-270-767-19820	Sequence 19820, A
280	20	0.7	297	4	US-09-270-767-23145	Sequence 23145, A	353	20	0.7	523	4	US-09-270-767-8076	Sequence 8076, App
281	20	0.7	297	4	US-09-248-796A-6983	Sequence 6983, App	354	20	0.7	523	4	US-09-270-767-23358	Sequence 23358, A
282	20	0.7	304	4	US-09-513-999C-23608	Sequence 23608, A	355	20	0.7	525	4	US-09-270-767-8915	Sequence 8915, App
283	20	0.7	313	4	US-09-621-976-9192	Sequence 9192, App	356	20	0.7	525	4	US-09-270-767-24197	Sequence 24197, A
284	20	0.7	316	4	US-09-513-999C-838	Sequence 838, App	357	20	0.7	525	4	US-09-270-767-26775	Sequence 26775, A
285	20	0.7	317	4	US-09-270-767-6919	Sequence 6919, App	C 358	20	0.7	526	4	US-09-220-132-164	Sequence 164, App
286	20	0.7	317	4	US-09-270-767-22201	Sequence 22201, A	359	20	0.7	527	4	US-09-621-976-14759	Sequence 14759, A
287	20	0.7	335	4	US-09-621-976-16658	Sequence 16658, A	360	20	0.7	530	2	US-08-605-106-8	Sequence 8, App1
288	20	0.7	337	3	US-09-328-111-586	Sequence 586, App	361	20	0.7	547	1	US-08-131-365B-41	Sequence 41, App1
289	20	0.7	342	3	US-09-385-982-342	Sequence 342, App	362	20	0.7	547	2	US-08-668-123-41	Sequence 41, App1
290	20	0.7	342	4	US-09-270-767-30251	Sequence 30251, A	363	20	0.7	547	4	US-09-621-976-11884	Sequence 11884, App
291	20	0.7	349	4	US-09-621-976-10564	Sequence 10564, A	C 364	20	0.7	567	3	US-09-385-982-427	Sequence 427, App
292	20	0.7	350	1	US-08-276-452A-62	Sequence 62, App1	365	20	0.7	567	4	US-09-246-963A-10	Sequence 10, App1
293	20	0.7	350	2	US-08-798-744-62	Sequence 62, App1	366	20	0.7	574	4	US-09-270-767-4270	Sequence 4270, App
294	20	0.7	354	4	US-09-270-767-26081	Sequence 26081, A	367	20	0.7	574	4	US-09-270-767-19552	Sequence 19552, A
295	20	0.7	360	3	US-08-888-077A-37	Sequence 37, App1	368	20	0.7	578	4	US-09-602-877A-95	Sequence 95, App1
296	20	0.7	362	4	US-09-621-976-16509	Sequence 16509, A	C 369	20	0.7	582	4	US-09-787-292-3	Sequence 3, App1
297	20	0.7	363	4	US-09-270-767-14764	Sequence 14764, A	370	20	0.7	587	1	US-08-313-681A-3	Sequence 3, App1
298	20	0.7	364	4	US-09-621-976-17462	Sequence 17462, A	371	20	0.7	587	3	US-09-322-911-3	Sequence 3, App1
299	20	0.7	367	4	US-09-621-976-16639	Sequence 16639, A	C 372	20	0.7	587	3	US-09-385-982-274	Sequence 274, App
300	20	0.7	367	4	US-09-270-767-5854	Sequence 5854, App	373	20	0.7	591	4	US-09-270-767-99598	Sequence 9958, App
301	20	0.7	367	4	US-09-270-767-21136	Sequence 21136, A	C 374	20	0.7	593	3	US-09-385-982-262	Sequence 262, App
302	20	0.7	381	3	US-09-091-725-32	Sequence 32, App1	375	20	0.7	596	1	US-08-150-331-45	Sequence 45, App1
303	20	0.7	381	4	US-09-621-976-16650	Sequence 16650, A	376	20	0.7	596	4	US-08-569-284-45	Sequence 45, App1
304	20	0.7	381	4	US-09-270-767-13106	Sequence 13106, A	377	20	0.7	599	3	US-09-256-000-12	Sequence 12, App1
305	20	0.7	387	4	US-09-408-087-1	Sequence 1, App1	378	20	0.7	599	4	US-10-034-015A-12	Sequence 12, App1
306	20	0.7	391	4	US-09-382-552-85	Sequence 85, App1	379	20	0.7	605	4	US-09-482-273-30	Sequence 30, App1
307	20	0.7	394	4	US-09-270-767-7596	Sequence 7596, App	C 380	20	0.7	607	3	US-09-385-982-288	Sequence 288, App
308	20	0.7	394	4	US-09-270-767-22878	Sequence 22878, A	381	20	0.7	616	4	US-09-270-767-9556	Sequence 9556, App
309	20	0.7	396	3	US-09-040-984-77	Sequence 77, App1	382	20	0.7	616	4	US-09-270-767-24638	Sequence 24638, A
310	20	0.7	396	3	US-09-123-912-77	Sequence 77, App1	383	20	0.7	618	1	US-07-912-900-26	Sequence 26, App1
311	20	0.7	396	4	US-09-643-597-77	Sequence 77, App1	384	20	0.7	618	1	US-08-285-309-26	Sequence 26, App1
312	20	0.7	396	4	US-09-480-884A-77	Sequence 77, App1	385	20	0.7	618	1	US-08-313-075A-33	Sequence 33, App1
313	20	0.7	396	4	US-09-542-615A-77	Sequence 77, App1	386	20	0.7	618	2	US-08-502-046-26	Sequence 26, App1
314	20	0.7	396	4	US-09-606-421B-77	Sequence 77, App1	387	20	0.7	620	4	US-09-270-767-11445	Sequence 11445, A
315	20	0.7	396	4	US-09-221-107-77	Sequence 77, App1	388	20	0.7	623	4	US-09-621-976-19162	Sequence 19162, A
316	20	0.7	396	4	US-09-466-396A-77	Sequence 77, App1	C 389	20	0.7	624	3	US-09-385-982-414	Sequence 414, App
317	20	0.7	396	4	US-09-270-767-28145	Sequence 28145, A	390	20	0.7	624	4	US-09-270-767-13424	Sequence 13424, A
318	20	0.7	396	4	US-09-476-496A-77	Sequence 77, App1	391	20	0.7	628	4	US-09-127-946-3	Sequence 3, App1
319	20	0.7	396	4	US-09-630-940B-77	Sequence 77, App1	C 392	20	0.7	629	3	US-09-385-982-389	Sequence 389, App

393	20	0.7	631	4	US-09-270-767-11978	Sequence 11978, A	466	20	0.7	854	3	US-09-247-155-67	Sequence 67, Appl
394	20	0.7	637	4	US-09-270-767-12204	Sequence 12204, A	467	20	0.7	855	3	US-08-906-769-130	Sequence 130, App
395	20	0.7	638	4	US-09-270-767-15026	Sequence 15026, A	468	20	0.7	855	3	US-08-906-616-130	Sequence 130, App
396	20	0.7	642	4	US-09-288-143-40	Sequence 40, Appl	469	20	0.7	855	3	US-08-639-075A-130	Sequence 130, App
397	20	0.7	645	4	US-09-270-767-5954	Sequence 5954, Ap	470	20	0.7	855	3	US-09-012-431-130	Sequence 130, App
398	20	0.7	645	4	US-09-270-767-21236	Sequence 21236, A	471	20	0.7	855	3	US-09-012-692-130	Sequence 130, App
399	20	0.7	658	4	US-09-465-559-1	Sequence 1, Appl	472	20	0.7	855	3	US-08-906-613-130	Sequence 130, App
400	20	0.7	659	4	US-09-311-021-157	Sequence 157, App	473	20	0.7	881	3	US-09-724-864-25	Sequence 25, Appl
401	20	0.7	665	4	US-09-780-717-52	Sequence 52, Appl	474	20	0.7	881	3	US-09-489-847-100	Sequence 100, App
402	20	0.7	676	2	US-08-533-669A-3	Sequence 3, Appl	475	20	0.7	896	4	US-09-171-209-5	Sequence 5, Appl
403	20	0.7	676	3	US-09-328-111-652	Sequence 652, App	476	20	0.7	897	4	US-08-899-330-14	Sequence 14, Appl
404	20	0.7	676	3	US-09-183-861-3	Sequence 3, Appl	477	20	0.7	898	4	US-09-270-767-6029	Sequence 6029, Ap
405	20	0.7	676	3	US-09-022-765-3	Sequence 3, Appl	478	20	0.7	898	4	US-09-270-767-21311	Sequence 21311, A
406	20	0.7	676	4	US-09-551-974A-3	Sequence 3, Appl	479	20	0.7	899	4	US-09-461-325-11	Sequence 11, Appl
407	20	0.7	676	4	US-09-565-501A-3	Sequence 3, Appl	480	20	0.7	899	4	US-10-012-542-11	Sequence 11, Appl
408	20	0.7	676	4	US-09-639-206A-3	Sequence 3, Appl	481	20	0.7	899	4	US-10-115-123-11	Sequence 11, Appl
409	20	0.7	676	4	US-09-874-923-3	Sequence 3, Appl	482	20	0.7	902	2	US-08-378-939-11	Sequence 11, Appl
410	20	0.7	676	4	US-08-798-841-3	Sequence 3, Appl	483	20	0.7	912	4	US-09-270-767-14143	Sequence 14143, A
411	20	0.7	680	4	US-09-489-674B-7	Sequence 7, Appl	484	20	0.7	914	3	US-09-227-357-123	Sequence 123, App
412	20	0.7	691	4	US-09-270-767-29557	Sequence 29557, A	485	20	0.7	927	4	US-09-270-767-1636	Sequence 1636, Ap
413	20	0.7	694	4	US-09-148-545-23	Sequence 23, Appl	486	20	0.7	927	4	US-09-270-767-19918	Sequence 19918, A
414	20	0.7	697	3	US-09-227-357-96	Sequence 96, Appl	487	20	0.7	931	3	US-08-924-747-9	Sequence 9, Appl
415	20	0.7	700	4	US-09-270-767-4977	Sequence 4977, Ap	488	20	0.7	931	3	US-09-247-373B-9	Sequence 9, Appl
416	20	0.7	700	4	US-09-270-767-20259	Sequence 20259, A	489	20	0.7	931	3	US-09-296-715-9	Sequence 9, Appl
417	20	0.7	705	4	US-09-465-559-3	Sequence 3, Appl	490	20	0.7	940	2	US-08-471-717-1	Sequence 1, Appl
418	20	0.7	716	4	US-09-270-767-9103	Sequence 9103, Ap	491	20	0.7	944	4	US-09-461-325-105	Sequence 105, App
419	20	0.7	716	4	US-09-270-767-24385	Sequence 24385, A	492	20	0.7	944	4	US-10-012-542-105	Sequence 105, App
420	20	0.7	730	3	US-09-352-990-3	Sequence 3, Appl	493	20	0.7	944	4	US-10-115-123-105	Sequence 105, App
421	20	0.7	732	3	US-08-923-454A-1	Sequence 1, Appl	494	20	0.7	952	1	US-08-181-271A-38	Sequence 38, Appl
422	20	0.7	734	4	US-09-270-767-10379	Sequence 10379, A	495	20	0.7	952	1	US-08-449-315-38	Sequence 38, Appl
423	20	0.7	737	2	US-08-691-814B-116	Sequence 116, App	496	20	0.7	952	1	US-08-444-803-38	Sequence 38, Appl
424	20	0.7	750	3	US-08-715-628B-2	Sequence 2, Appl	497	20	0.7	952	1	US-08-444-043-38	Sequence 38, Appl
425	20	0.7	750	3	US-09-553-769-1	Sequence 1, Appl	498	20	0.7	952	1	US-08-456-265A-38	Sequence 38, Appl
426	20	0.7	753	3	US-09-232-191-14	Sequence 14, Appl	499	20	0.7	952	1	US-08-455-416-38	Sequence 38, Appl
427	20	0.7	753	3	US-09-232-200-14	Sequence 14, Appl	500	20	0.7	952	1	US-08-455-244-38	Sequence 38, Appl
428	20	0.7	753	3	US-09-232-197-14	Sequence 14, Appl	501	20	0.7	952	1	US-08-454-876-38	Sequence 38, Appl
429	20	0.7	753	3	US-09-232-201-14	Sequence 14, Appl	502	20	0.7	952	2	US-08-457-364-38	Sequence 38, Appl
430	20	0.7	753	4	US-09-232-195-14	Sequence 14, Appl	503	20	0.7	952	2	US-08-456-262-38	Sequence 38, Appl
431	20	0.7	753	4	US-09-302-331B-9	Sequence 9, Appl	504	20	0.7	952	2	US-08-456-240-38	Sequence 38, Appl
432	20	0.7	755	4	US-09-621-976-1858	Sequence 1858, Ap	505	20	0.7	952	2	US-08-455-736-38	Sequence 38, Appl
433	20	0.7	756	4	US-09-614-912-93	Sequence 93, Appl	506	20	0.7	952	2	US-08-971-217-38	Sequence 38, Appl
434	20	0.7	767	1	US-07-697-275-1	Sequence 1, Appl	507	20	0.7	952	3	US-09-350-600-38	Sequence 38, Appl
435	20	0.7	767	4	US-08-400-421-1	Sequence 1, Appl	508	20	0.7	952	4	US-09-906-234-38	Sequence 38, Appl
436	20	0.7	768	4	US-09-620-312D-707	Sequence 707, App	509	20	0.7	954	1	US-08-315-695-15	Sequence 15, Appl
437	20	0.7	775	4	US-09-780-717-16	Sequence 16, Appl	510	20	0.7	960	3	US-09-248-335-57	Sequence 57, Appl
438	20	0.7	777	3	US-09-385-982-531	Sequence 531, App	511	20	0.7	961	4	US-09-149-476-84	Sequence 84, App
439	20	0.7	783	2	US-08-851-822A-2	Sequence 2, Appl	512	20	0.7	975	4	US-09-270-767-6872	Sequence 6872, App
440	20	0.7	783	2	US-09-184-384-2	Sequence 2, Appl	513	20	0.7	975	4	US-09-270-767-22154	Sequence 22154, A
441	20	0.7	785	4	US-09-518-036-9	Sequence 9, Appl	514	20	0.7	981	3	US-08-815-225-1	Sequence 1, Appl
442	20	0.7	785	4	US-10-279-130-9	Sequence 9, Appl	515	20	0.7	991	4	US-09-344-529-3	Sequence 3, Appl
443	20	0.7	787	4	US-09-621-976-1878	Sequence 1878, Ap	516	20	0.7	994	4	US-09-366-887A-5	Sequence 5, Appl
444	20	0.7	793	4	US-09-311-021-39	Sequence 39, Appl	517	20	0.7	994	4	US-09-517-204-5	Sequence 5, Appl
445	20	0.7	794	4	US-09-173-300-10	Sequence 10, Appl	518	20	0.7	1001	3	US-08-983-409-4	Sequence 4, Appl
446	20	0.7	800	4	US-09-270-767-10958	Sequence 10958, A	519	20	0.7	1016	2	US-08-909-965C-2	Sequence 2, Appl
447	20	0.7	806	3	US-08-906-769-120	Sequence 120, App	520	20	0.7	1020	4	US-09-328-475C-43	Sequence 43, Appl
448	20	0.7	806	3	US-08-906-616-120	Sequence 120, App	521	20	0.7	1021	4	US-09-149-476-145	Sequence 145, App
449	20	0.7	806	3	US-08-639-075A-120	Sequence 120, App	522	20	0.7	1023	4	US-09-228-947-38	Sequence 38, Appl
450	20	0.7	806	3	US-09-012-431-120	Sequence 120, App	523	20	0.7	1027	4	US-09-344-529-1	Sequence 1, Appl
451	20	0.7	806	3	US-09-012-692-120	Sequence 120, App	524	20	0.7	1027	4	US-09-465-558-57	Sequence 57, Appl
452	20	0.7	806	3	US-08-906-613-120	Sequence 120, App	525	20	0.7	1036	3	US-09-267-031-9	Sequence 9, Appl
453	20	0.7	806	1	US-08-441-629-1	Sequence 1, Appl	526	20	0.7	1047	4	US-09-096-724B-17	Sequence 17, Appl
454	20	0.7	809	3	US-08-776-207-1	Sequence 1, Appl	527	20	0.7	1049	4	US-09-800-729-67	Sequence 67, Appl
455	20	0.7	809	3	US-09-507-773-1	Sequence 1, Appl	528	20	0.7	1051	4	US-09-396-149-15	Sequence 15, Appl
456	20	0.7	809	5	PCT-US95-09172-1	Sequence 1, Appl	529	20	0.7	1052	4	US-09-270-767-11904	Sequence 11904, A
457	20	0.7	812	4	US-09-311-021-43	Sequence 43, Appl	530	20	0.7	1060	4	US-09-691-270A-9	Sequence 9, Appl
458	20	0.7	815	4	US-09-288-143-24	Sequence 24, Appl	531	20	0.7	1061	4	US-09-489-847-88	Sequence 88, Appl
459	20	0.7	818	4	US-09-328-475C-116	Sequence 116, App	532	20	0.7	1062	4	US-09-244-111-1	Sequence 1, Appl
460	20	0.7	830	3	US-09-227-357-64	Sequence 64, Appl	533	20	0.7	1064	4	US-09-036-724B-18	Sequence 18, Appl
461	20	0.7	830	3	US-09-227-357-147	Sequence 147, App	534	20	0.7	1066	4	US-09-886-319A-51	Sequence 51, Appl
462	20	0.7	831	4	US-09-205-258-75	Sequence 75, Appl	535	20	0.7	1068	4	US-09-270-767-12721	Sequence 12721, A
463	20	0.7	831	4	US-09-894-916-6	Sequence 6, Appl	536	20	0.7	1069	2	US-08-768-964-1	Sequence 1, Appl
464	20	0.7	845	4	US-09-270-767-26060	Sequence 26060, A	537	20	0.7	1069	2	US-08-768-964-3	Sequence 3, Appl
465	20	0.7	849	3	US-09-227-357-72	Sequence 72, Appl	538	20	0.7	1069	3	US-09-005-299-1	Sequence 1, Appl

C 539	20	0.7	1069	3	US-09-005-299-3	Sequence 3, Appl1	612	20	0.7	1316	5	PCT-US95-12509-12	Sequence 12, Appl1
540	20	0.7	1069	3	US-09-515-431-1	Sequence 1, Appl1	613	20	0.7	1318	4	US-09-719-108-1	Sequence 1, Appl1
C 541	20	0.7	1069	3	US-09-515-431-3	Sequence 3, Appl1	614	20	0.7	1318	4	US-09-393-634-2	Sequence 2, Appl1
542	20	0.7	1071	4	US-09-248-796A-7112	Sequence 7112, Ap	615	20	0.7	1338	3	US-09-027-064-3	Sequence 3, Appl1
543	20	0.7	1076	4	US-09-690-454-17	Sequence 17, Appl	616	20	0.7	1338	3	US-09-271-815-3	Sequence 3, Appl1
544	20	0.7	1079	4	US-10-074-509-1	Sequence 1, Appl1	617	20	0.7	1366	4	US-09-770-767-13559	Sequence 13559, A
545	20	0.7	1081	2	US-09-090-567-1	Sequence 1, Appl1	618	20	0.7	1360	4	US-09-856-599-2	Sequence 2, Appl1
546	20	0.7	1091	4	US-09-270-767-10251	Sequence 10251, A	C 619	20	0.7	1361	4	US-09-489-847-64	Sequence 64, Appl
547	20	0.7	1099	4	US-09-533-029-1	Sequence 1, Appl1	620	20	0.7	1386	3	US-09-364-230-23	Sequence 23, Appl
548	20	0.7	1102	3	US-08-726-807B-8	Sequence 8, Appl1	621	20	0.7	1389	4	US-09-501-115-11	Sequence 11, Appl
549	20	0.7	1102	3	US-09-258-367-8	Sequence 8, Appl1	622	20	0.7	1391	4	US-09-149-476-44	Sequence 44, Appl
550	20	0.7	1102	3	US-09-546-550-8	Sequence 8, Appl1	623	20	0.7	1395	4	US-09-311-021-205	Sequence 205, App
551	20	0.7	1102	3	US-09-431-414-8	Sequence 8, Appl1	624	20	0.7	1397	4	US-09-270-767-11144	Sequence 1144, A
552	20	0.7	1102	3	US-09-225-670-8	Sequence 8, Appl1	625	20	0.7	1400	4	US-09-305-258-23	Sequence 238, App
553	20	0.7	1102	3	US-09-431-349C-8	Sequence 8, Appl1	626	20	0.7	1411	4	US-09-370-838-154	Sequence 154, App
554	20	0.7	1107	4	US-09-270-767-11743	Sequence 11743, A	627	20	0.7	1411	4	US-09-854-133-154	Sequence 154, App
555	20	0.7	1113	4	US-09-461-325-97	Sequence 97, Appl	628	20	0.7	1413	3	US-09-504-445-1	Sequence 1, Appl1
556	20	0.7	1113	4	US-10-012-542-97	Sequence 97, Appl	629	20	0.7	1414	4	US-09-270-767-15271	Sequence 15271, A
557	20	0.7	1113	4	US-10-115-123-97	Sequence 97, Appl	630	20	0.7	1417	2	US-08-713-828-2	Sequence 2, Appl1
558	20	0.7	1146	4	US-09-452-239-3	Sequence 3, Appl1	631	20	0.7	1417	2	US-08-919-627-2	Sequence 2, Appl1
559	20	0.7	1160	4	US-09-270-767-1071	Sequence 1071, Ap	632	20	0.7	1417	2	US-09-096-245-2	Sequence 2, Appl1
560	20	0.7	1160	4	US-09-387-341-215	Sequence 16353, A	633	20	0.7	1423	4	US-09-461-325-51	Sequence 51, Appl
561	20	0.7	1165	3	US-09-091-725-20	Sequence 20, Appl	634	20	0.7	1423	4	US-10-012-542-51	Sequence 51, Appl
562	20	0.7	1169	4	US-09-690-454-11	Sequence 11, Appl	635	20	0.7	1423	4	US-09-735-846-21	Sequence 21, Appl
563	20	0.7	1174	4	US-10-164-595-49	Sequence 49, Appl	636	20	0.7	1423	4	US-10-115-123-51	Sequence 51, Appl
C 564	20	0.7	1175	4	US-09-387-341-215	Sequence 215, App	637	20	0.7	1439	4	US-09-668-097A-25	Sequence 25, Appl
565	20	0.7	1208	4	US-09-461-325-14	Sequence 14, Appl	638	20	0.7	1445	3	US-09-814-951A-1	Sequence 1, Appl1
566	20	0.7	1208	4	US-10-012-542-14	Sequence 14, Appl	639	20	0.7	1448	1	US-08-298-426-1	Sequence 1, Appl1
567	20	0.7	1208	4	US-10-115-123-14	Sequence 14, Appl	640	20	0.7	1450	4	US-09-599-360B-24	Sequence 24, Appl
568	20	0.7	1211	2	US-08-379-556A-1	Sequence 1, Appl1	641	20	0.7	1458	4	US-09-311-021-201	Sequence 201, App
C 569	20	0.7	1211	4	US-09-270-767-6328	Sequence 6328, Ap	642	20	0.7	1460	4	US-09-370-838-80	Sequence 80, Appl
C 570	20	0.7	1211	4	US-09-270-767-21610	Sequence 21610, A	643	20	0.7	1460	4	US-09-854-133-80	Sequence 80, Appl
571	20	0.7	1225	1	US-08-286-020-1	Sequence 1, Appl1	644	20	0.7	1462	4	US-09-370-838-55	Sequence 55, Appl
572	20	0.7	1225	1	US-08-603-919-1	Sequence 1, Appl1	645	20	0.7	1462	4	US-09-854-133-55	Sequence 55, Appl
573	20	0.7	1227	1	US-08-080-386-1	Sequence 1, Appl1	C 646	20	0.7	1462	4	US-09-854-133-55	Sequence 55, Appl
574	20	0.7	1227	2	US-08-390-000A-1	Sequence 1, Appl1	647	20	0.7	1497	4	US-09-270-767-10652	Sequence 10652, A
575	20	0.7	1233	4	US-09-856-486-13	Sequence 13, Appl	C 648	20	0.7	1498	4	US-09-220-132-94	Sequence 94, Appl
576	20	0.7	1236	4	US-09-918-686-19	Sequence 19, Appl	649	20	0.7	1510	1	US-09-270-767-15231	Sequence 15231, A
577	20	0.7	1243	4	US-09-731-924A-1	Sequence 1, Appl1	650	20	0.7	1510	4	US-07-759-568-4	Sequence 4, Appl1
578	20	0.7	1244	4	US-08-916-442-1	Sequence 1, Appl1	651	20	0.7	1513	4	US-09-023-655-1140	Sequence 1140, Ap
579	20	0.7	1244	4	US-09-317-641-1	Sequence 1, Appl1	652	20	0.7	1514	3	US-09-716-129-23	Sequence 23, Appl
580	20	0.7	1250	4	US-09-311-021-37	Sequence 37, Appl	653	20	0.7	1531	4	US-08-675-816-1	Sequence 1, Appl1
C 581	20	0.7	1253	4	US-09-673-395A-71	Sequence 71, Appl	C 654	20	0.7	1531	4	US-09-270-767-5166	Sequence 5166, Ap
C 582	20	0.7	1266	4	US-09-270-767-6939	Sequence 6939, Ap	655	20	0.7	1533	1	US-09-270-767-20448	Sequence 20448, A
C 583	20	0.7	1266	4	US-09-370-767-22321	Sequence 22321, A	656	20	0.7	1533	2	US-08-485-938A-23	Sequence 23, Appl
584	20	0.7	1268	4	US-09-461-325-126	Sequence 126, App	657	20	0.7	1533	2	US-08-910-041-23	Sequence 23, Appl
585	20	0.7	1268	4	US-10-012-542-126	Sequence 126, App	658	20	0.7	1533	3	US-09-328-474-23	Sequence 23, Appl
586	20	0.7	1268	4	US-10-115-123-126	Sequence 126, App	659	20	0.7	1533	3	US-09-100-546-23	Sequence 23, Appl
587	20	0.7	1271	4	US-09-270-767-11058	Sequence 11058, A	660	20	0.7	1533	3	US-09-010-715-23	Sequence 23, Appl
C 588	20	0.7	1271	4	US-09-270-767-11058	Sequence 11058, A	661	20	0.7	1533	3	US-09-577-758-23	Sequence 23, Appl
589	20	0.7	1271	4	US-09-187-999-30	Sequence 30, Appl	662	20	0.7	1533	3	US-09-577-758-23	Sequence 23, Appl
590	20	0.7	1281	4	US-09-620-312D-972	Sequence 972, App	663	20	0.7	1534	3	US-09-399-914-7	Sequence 7, Appl1
591	20	0.7	1284	3	US-09-286-529-6	Sequence 6, Appl1	664	20	0.7	1534	3	US-09-298-731-7	Sequence 7, Appl1
592	20	0.7	1286	4	US-09-489-847-124	Sequence 124, App	665	20	0.7	1534	4	US-09-489-847-110	Sequence 110, App
593	20	0.7	1291	4	US-09-904-615-17	Sequence 17, Appl	666	20	0.7	1541	4	US-09-350-614-7	Sequence 7, Appl1
594	20	0.7	1292	4	US-09-904-615-61	Sequence 61, Appl	667	20	0.7	1542	4	US-09-489-847-24	Sequence 24, Appl
C 595	20	0.7	1297	4	US-09-004-730A-114	Sequence 114, App	668	20	0.7	1542	4	US-09-270-767-14570	Sequence 14570, A
C 596	20	0.7	1297	4	US-09-004-730A-116	Sequence 116, App	669	20	0.7	1543	3	US-09-227-357-26	Sequence 26, Appl
C 597	20	0.7	1297	4	US-08-981-799A-114	Sequence 116, App	670	20	0.7	1545	4	US-09-559-023-1	Sequence 1, Appl1
C 598	20	0.7	1297	4	US-08-981-799A-114	Sequence 116, App	671	20	0.7	1545	4	US-09-444-336-5	Sequence 5, Appl1
C 599	20	0.7	1299	1	US-08-463-262A-11	Sequence 116, App	672	20	0.7	1558	4	US-09-369-247-37	Sequence 37, Appl
C 600	20	0.7	1299	1	US-08-463-262A-11	Sequence 1, Appl1	673	20	0.7	1560	3	US-09-261-599B-5	Sequence 5, Appl1
C 601	20	0.7	1299	3	US-08-721-986-8	Sequence 8, Appl1	674	20	0.7	1560	3	US-09-456-455A-5	Sequence 5, Appl1
602	20	0.7	1299	3	US-08-225-487A-8	Sequence 8, Appl1	675	20	0.7	1574	4	US-09-246-963A-5	Sequence 5, Appl1
C 603	20	0.7	1299	3	US-09-003-574-1	Sequence 1, Appl1	676	20	0.7	1575	4	US-09-561-763-4	Sequence 4, Appl1
C 604	20	0.7	1299	3	US-09-003-570-1	Sequence 1, Appl1	677	20	0.7	1575	4	US-09-431-367B-4	Sequence 4, Appl1
C 605	20	0.7	1299	4	US-09-864-541A-1	Sequence 1, Appl1	678	20	0.7	1578	3	US-09-560-761-23	Sequence 23, Appl
C 606	20	0.7	1314	4	US-09-644-907B-1	Sequence 1, Appl1	679	20	0.7	1578	3	US-09-044-404A-1	Sequence 1, Appl1
607	20	0.7	1316	1	US-08-315-831A-12	Sequence 12, Appl	680	20	0.7	1584	4	US-09-586-924-1	Sequence 1, Appl1
608	20	0.7	1316	1	US-08-662-318-12	Sequence 12, Appl	681	20	0.7	1584	4	US-09-807-258-11	Sequence 11, Appl
609	20	0.7	1316	1	US-09-362-123A-1	Sequence 1, Appl1	682	20	0.7	1590	3	US-09-280-428A-5	Sequence 5, Appl1
C 610	20	0.7	1316	4	US-09-270-767-2481	Sequence 2481, Ap	683	20	0.7	1594	4	US-09-227-357-12	Sequence 12, Appl
C 611	20	0.7	1316	4	US-09-270-767-17763	Sequence 17763, A	684	20	0.7	1605	4	US-09-016-643-1059	Sequence 1059, Ap

685	20	0.7	1606	4	US-09-620-312D-99	Sequence 99, Appl	758	20	0.7	1860	3	US-09-071-444-2	Sequence 2, Appl
686	20	0.7	1613	4	US-09-270-767-10620	Sequence 10620, A	759	20	0.7	1860	4	US-09-919-039-347	Sequence 347, App
687	20	0.7	1619	4	US-09-799-451-640	Sequence 640, App	760	20	0.7	1865	4	US-09-819-607-1	Sequence 1, Appl
688	20	0.7	1621	3	US-09-020-956-107	Sequence 107, App	761	20	0.7	1865	4	US-09-722-971-13	Sequence 13, Appl
689	20	0.7	1621	3	US-09-030-607-107	Sequence 107, App	762	20	0.7	1883	3	US-10-140-002-501	Sequence 501, App
690	20	0.7	1621	3	US-09-439-313-107	Sequence 107, App	763	20	0.7	1889	3	US-09-187-050-1	Sequence 1, Appl
691	20	0.7	1621	3	US-09-352-616A-107	Sequence 107, App	764	20	0.7	1895	4	US-09-444-336-7	Sequence 7, Appl
692	20	0.7	1621	4	US-09-232-149A-107	Sequence 107, App	765	20	0.7	1904	3	US-09-399-913-29	Sequence 29, Appl
693	20	0.7	1621	4	US-09-159-812-107	Sequence 107, App	766	20	0.7	1904	3	US-09-298-731-29	Sequence 29, Appl
694	20	0.7	1621	4	US-09-636-215-107	Sequence 107, App	767	20	0.7	1904	4	US-09-350-614-29	Sequence 29, Appl
695	20	0.7	1621	4	US-09-685-166A-107	Sequence 107, App	768	20	0.7	1913	4	US-09-461-325-470	Sequence 470, App
696	20	0.7	1621	4	US-09-115-453-107	Sequence 107, App	769	20	0.7	1913	4	US-10-012-542-470	Sequence 470, App
697	20	0.7	1621	4	US-09-688-489-107	Sequence 107, App	770	20	0.7	1913	4	US-10-115-123-470	Sequence 470, App
698	20	0.7	1621	4	US-09-679-426-107	Sequence 107, App	771	20	0.7	1921	2	US-08-557-128-11	Sequence 11, Appl
699	20	0.7	1622	3	US-09-004-393B-1	Sequence 1, Appl	772	20	0.7	1928	4	US-09-723-368-1	Sequence 1, Appl
700	20	0.7	1627	4	US-09-485-473-4	Sequence 4, Appl	773	20	0.7	1928	4	US-08-754-477A-117	Sequence 117, App
701	20	0.7	1630	4	US-09-673-395A-59	Sequence 59, Appl	774	20	0.7	1929	4	US-08-754-477A-118	Sequence 118, App
702	20	0.7	1634	4	US-08-928-069-11	Sequence 11, Appl	775	20	0.7	1929	4	US-08-754-477A-123	Sequence 123, App
703	20	0.7	1634	4	US-08-828-683A-9	Sequence 9, Appl	776	20	0.7	1929	4	US-08-754-477A-127	Sequence 127, App
704	20	0.7	1637	4	US-09-270-767-11283	Sequence 11283, A	777	20	0.7	1929	4	US-08-754-477A-128	Sequence 128, App
705	20	0.7	1638	3	US-09-833-553-1	Sequence 1, Appl	778	20	0.7	1929	4	US-08-754-477A-129	Sequence 129, App
706	20	0.7	1638	3	US-09-078-173A-12	Sequence 12, Appl	779	20	0.7	1929	4	US-08-754-477A-133	Sequence 133, App
707	20	0.7	1638	3	US-09-418-223-1	Sequence 1, Appl	780	20	0.7	1929	4	US-08-754-477A-137	Sequence 137, App
708	20	0.7	1638	4	US-10-042-991-12	Sequence 12, Appl	781	20	0.7	1930	4	US-09-016-434-1171	Sequence 1171, Ap
709	20	0.7	1645	4	US-09-311-021-121	Sequence 121, App	782	20	0.7	1931	4	US-09-461-325-85	Sequence 85, Appl
710	20	0.7	1646	4	US-09-443-041A-19	Sequence 19, Appl	783	20	0.7	1931	4	US-10-012-542-85	Sequence 85, Appl
711	20	0.7	1647	4	US-09-535-909-1	Sequence 1, Appl	784	20	0.7	1931	4	US-10-115-123-85	Sequence 109, App
712	20	0.7	1683	3	US-09-347-803-11	Sequence 11, Appl	785	20	0.7	1932	4	US-09-489-847-109	Sequence 109, App
713	20	0.7	1701	1	US-07-863-169A-2	Sequence 2, Appl	786	20	0.7	1935	4	US-09-270-767-10639	Sequence 10639, A
714	20	0.7	1701	2	US-08-429-964-2	Sequence 2, Appl	787	20	0.7	1937	4	US-09-270-767-12385	Sequence 12385, A
715	20	0.7	1701	2	US-09-357-072-1	Sequence 1, Appl	788	20	0.7	1947	4	US-09-489-847-26	Sequence 26, Appl
716	20	0.7	1701	3	US-07-935-087-2	Sequence 1, Appl	789	20	0.7	1957	4	US-09-489-847-98	Sequence 98, Appl
717	20	0.7	1701	3	US-08-983-502-1	Sequence 1, Appl	790	20	0.7	1959	3	US-09-166-460-1	Sequence 1, Appl
718	20	0.7	1701	4	US-09-516-747-1	Sequence 2, Appl	791	20	0.7	1959	4	US-09-361-718-1	Sequence 27, Appl
719	20	0.7	1701	5	PCT-US93-08062-2	Sequence 1, Appl	792	20	0.7	1959	4	US-09-398-395A-27	Sequence 27, Appl
720	20	0.7	1701	5	PCT-US95-16542-1	Sequence 1, Appl	793	20	0.7	1959	4	US-09-887-586A-27	Sequence 27, Appl
721	20	0.7	1702	4	PCT-US86-10521-1	Sequence 1, Appl	794	20	0.7	1959	4	US-09-895-752-27	Sequence 27, Appl
722	20	0.7	1702	4	US-09-023-655-1391	Sequence 1391, App	795	20	0.7	1959	4	US-09-903-012B-27	Sequence 27, Appl
723	20	0.7	1712	4	US-09-148-545-106	Sequence 106, App	796	20	0.7	1959	4	US-09-900-797-27	Sequence 27, Appl
724	20	0.7	1718	4	US-09-778-510-5	Sequence 5, Appl	797	20	0.7	1960	4	US-09-679-666B-15	Sequence 15, Appl
725	20	0.7	1727	4	US-09-327-983-3	Sequence 3, Appl	798	20	0.7	1962	4	US-09-673-395A-541	Sequence 541, App
726	20	0.7	1731	4	US-09-600-588-2	Sequence 2, Appl	799	20	0.7	1964	1	US-08-132-168A-31	Sequence 31, Appl
727	20	0.7	1753	4	US-09-436-699C-15	Sequence 15, Appl	800	20	0.7	1967	4	US-09-398-395A-23	Sequence 23, Appl
728	20	0.7	1754	4	US-09-604-978-1	Sequence 1, Appl	801	20	0.7	1967	4	US-09-887-586A-23	Sequence 23, Appl
729	20	0.7	1754	4	US-09-604-978-1	Sequence 1, Appl	802	20	0.7	1967	4	US-09-895-752-23	Sequence 23, Appl
730	20	0.7	1756	4	US-10-325-878-1	Sequence 1, Appl	803	20	0.7	1967	4	US-09-903-012B-23	Sequence 23, Appl
731	20	0.7	1756	4	US-09-614-912-117	Sequence 117, App	804	20	0.7	1967	4	US-09-900-797-23	Sequence 23, Appl
732	20	0.7	1757	4	US-09-489-847-12	Sequence 12, App	805	20	0.7	1968	2	US-08-937-540-3	Sequence 3, Appl
733	20	0.7	1770	3	US-08-943-731-146	Sequence 146, App	806	20	0.7	2017	4	US-09-270-767-12457	Sequence 12457, A
734	20	0.7	1775	4	US-08-754-477A-1	Sequence 1, Appl	807	20	0.7	2019	4	US-09-673-395A-53	Sequence 53, Appl
735	20	0.7	1775	4	US-08-754-477A-4	Sequence 4, Appl	808	20	0.7	2034	4	US-09-489-847-83	Sequence 83, Appl
736	20	0.7	1775	4	US-08-754-477A-120	Sequence 120, App	809	20	0.7	2047	4	US-09-270-767-11235	Sequence 11235, A
737	20	0.7	1775	4	US-08-754-477A-124	Sequence 124, App	810	20	0.7	2051	3	US-09-399-913-52	Sequence 52, Appl
738	20	0.7	1775	4	US-08-754-477A-130	Sequence 130, App	811	20	0.7	2051	3	US-09-350-614-52	Sequence 52, Appl
739	20	0.7	1775	4	US-08-754-477A-134	Sequence 134, App	812	20	0.7	2056	3	US-09-334-601-12	Sequence 12, Appl
740	20	0.7	1782	4	US-09-604-978-2	Sequence 2, Appl	813	20	0.7	2057	3	US-09-399-913-27	Sequence 27, Appl
741	20	0.7	1782	4	US-09-604-978-2	Sequence 2, Appl	814	20	0.7	2057	3	US-09-399-913-41	Sequence 41, Appl
742	20	0.7	1782	4	US-10-325-878-2	Sequence 2, Appl	815	20	0.7	2057	4	US-09-298-731-27	Sequence 27, Appl
743	20	0.7	1783	3	US-08-815-469-1	Sequence 1, Appl	816	20	0.7	2057	4	US-09-350-614-27	Sequence 27, Appl
744	20	0.7	1783	4	US-09-557-908-1	Sequence 1, Appl	817	20	0.7	2057	4	US-09-350-614-41	Sequence 41, Appl
745	20	0.7	1783	4	US-09-333-966-1	Sequence 1, Appl	818	20	0.7	2060	3	US-09-370-807-1	Sequence 1, Appl
746	20	0.7	1785	4	US-09-216-393B-311	Sequence 311, App	819	20	0.7	2060	4	US-09-921-250-1	Sequence 1, Appl
747	20	0.7	1785	4	US-09-216-393B-313	Sequence 313, App	820	20	0.7	2065	2	US-08-968-751-1	Sequence 1, Appl
748	20	0.7	1799	3	US-09-329-633A-1	Sequence 1, Appl	821	20	0.7	2118	4	US-09-690-454-16	Sequence 16, Appl
749	20	0.7	1799	3	US-09-079-029-2	Sequence 2, Appl	822	20	0.7	2119	4	US-09-399-588-1	Sequence 1, Appl
750	20	0.7	1810	4	US-09-369-247-11	Sequence 11, Appl	823	20	0.7	2121	1	US-08-331-394-3	Sequence 3, Appl
751	20	0.7	1819	2	US-08-371-377-20	Sequence 20, Appl	824	20	0.7	2121	1	US-08-250-858-3	Sequence 3, Appl
752	20	0.7	1820	4	US-09-778-510-1	Sequence 1, Appl	825	20	0.7	2121	1	US-08-446-915-3	Sequence 3, Appl
753	20	0.7	1822	4	US-09-148-545-105	Sequence 105, App	826	20	0.7	2121	2	US-08-744-139-3	Sequence 3, Appl
754	20	0.7	1823	3	US-08-535-276-2	Sequence 2, Appl	827	20	0.7	2121	4	US-08-779-599-3	Sequence 3, Appl
755	20	0.7	1823	3	US-09-335-234-2	Sequence 2, Appl	828	20	0.7	2121	5	PCT-US95-06639-3	Sequence 3, Appl
756	20	0.7	1829	2	US-08-687-080-57	Sequence 57, Appl	829	20	0.7	2128	4	US-09-673-395A-532	Sequence 532, App
757	20	0.7	1854	3	US-09-724-864-29	Sequence 29, Appl	830	20	0.7	2131	1	US-08-325-071-64	Sequence 64, Appl

831	20	0.7	2131	3	US-08-461-004A-64	Sequence 64, Appl	904	20	0.7	2501	3	US-08-787-739-58	Sequence 58, Appl
832	20	0.7	2134	4	US-09-629-222A-23	Sequence 23, Appl	905	20	0.7	2501	3	US-09-178-115-58	Sequence 58, Appl
833	20	0.7	2140	3	US-09-058-389A-6	Sequence 6, Appl1	906	20	0.7	2501	3	US-09-177-77E-58	Sequence 58, Appl
834	20	0.7	2140	4	US-09-611-781-6	Sequence 6, Appl1	907	20	0.7	2525	3	US-09-234-393-39	Sequence 39, Appl
835	20	0.7	2152	4	US-09-629-222A-1	Sequence 1, Appl1	908	20	0.7	2525	4	US-09-865-171-39	Sequence 39, Appl
836	20	0.7	2152	4	US-09-629-222A-25	Sequence 25, Appl	909	20	0.7	2528	3	US-09-234-393-37	Sequence 37, Appl
837	20	0.7	2152	4	US-09-629-222A-26	Sequence 26, Appl	910	20	0.7	2528	4	US-09-234-393-41	Sequence 41, Appl
838	20	0.7	2152	4	US-09-629-222A-27	Sequence 27, Appl	911	20	0.7	2528	4	US-09-865-171-37	Sequence 37, Appl
839	20	0.7	2196	1	US-08-245-809-2	Sequence 2, Appl1	912	20	0.7	2528	4	US-09-865-171-41	Sequence 41, Appl
840	20	0.7	2199	1	US-08-107-748-1	Sequence 1, Appl1	913	20	0.7	2542	1	US-08-120-960-1	Sequence 1, Appl1
841	20	0.7	2199	5	PCT-US92-01385-1	Sequence 1, Appl1	914	20	0.7	2542	1	US-09-347-878-8	Sequence 8, Appl1
842	20	0.7	2207	4	US-10-140-002-137	Sequence 137, App	915	20	0.7	2543	4	US-09-614-912-21	Sequence 21, Appl
843	20	0.7	2214	4	US-10-327-189-1	Sequence 1, Appl1	916	20	0.7	2570	20	US-09-270-767-13498	Sequence 13498, A
844	20	0.7	2236	3	US-09-239-966-3	Sequence 3, Appl1	917	20	0.7	2571	3	US-09-234-393-12	Sequence 12, Appl
845	20	0.7	2242	4	US-09-738-946-9	Sequence 9, Appl1	918	20	0.7	2571	4	US-09-865-171-12	Sequence 12, Appl
846	20	0.7	2259	4	US-10-067-422-2	Sequence 2, Appl1	919	20	0.7	2578	4	US-09-124-398-8	Sequence 8, Appl1
847	20	0.7	2271	4	US-09-904-615-52	Sequence 52, Appl	920	20	0.7	2639	3	US-09-374-135-1	Sequence 1, Appl1
848	20	0.7	2271	3	US-09-332-191-10	Sequence 10, Appl	921	20	0.7	2640	4	US-09-857-447-3	Sequence 1, Appl1
849	20	0.7	2277	3	US-09-332-200-10	Sequence 10, Appl	922	20	0.7	2640	4	US-09-857-447-3	Sequence 1, Appl1
850	20	0.7	2277	3	US-09-332-200-72	Sequence 10, Appl	923	20	0.7	2643	2	US-08-750-134A-10	Sequence 10, Appl
851	20	0.7	2277	3	US-09-332-197-10	Sequence 10, Appl	924	20	0.7	2643	3	US-09-363-74E-10	Sequence 10, Appl
852	20	0.7	2277	3	US-09-332-197-72	Sequence 72, Appl	925	20	0.7	2643	4	US-09-023-658-897	Sequence 897, App
853	20	0.7	2277	3	US-09-332-201-10	Sequence 10, Appl	926	20	0.7	2685	3	US-09-061-768A-1	Sequence 1, Appl1
854	20	0.7	2277	3	US-09-332-201-72	Sequence 72, Appl	927	20	0.7	2685	4	US-09-764-246-1	Sequence 1, Appl1
855	20	0.7	2277	4	US-09-332-195-10	Sequence 10, Appl	928	20	0.7	2695	4	US-09-706-197-3	Sequence 3, Appl1
856	20	0.7	2294	4	US-08-367-508-10	Sequence 72, Appl	929	20	0.7	2721	3	US-08-921-195-1	Sequence 1, Appl1
857	20	0.7	2294	2	US-08-967-506-10	Sequence 10, Appl	930	20	0.7	2740	4	US-09-973-963-3	Sequence 3, Appl1
858	20	0.7	2294	3	PCT-US94-02552-10	Sequence 10, Appl	931	20	0.7	2797	4	US-09-482-273-74	Sequence 74, Appl
859	20	0.7	2294	5	US-09-399-913-21	Sequence 21, Appl	932	20	0.7	2811	1	US-08-040-548-31	Sequence 31, Appl
860	20	0.7	2300	3	US-09-298-731-21	Sequence 21, Appl	933	20	0.7	2811	1	US-08-466-344-31	Sequence 31, Appl
861	20	0.7	2300	4	US-09-350-614-21	Sequence 21, Appl	934	20	0.7	2817	1	US-08-655-836-4	Sequence 4, Appl1
862	20	0.7	2300	1	US-08-464-266-1	Sequence 1, Appl1	935	20	0.7	2817	2	US-09-020-755-4	Sequence 4, Appl1
863	20	0.7	2304	1	US-08-464-266-1	Sequence 1, Appl1	936	20	0.7	2817	6	5206152-6	Patent No. 5206152
864	20	0.7	2304	1	US-08-464-514-1	Sequence 1, Appl1	937	20	0.7	2834	1	US-08-471-251A-1	Sequence 1, Appl1
865	20	0.7	2304	3	US-08-464-514-1	Sequence 1, Appl1	938	20	0.7	2880	3	US-09-115-954-3	Sequence 3, Appl1
866	20	0.7	2304	3	US-08-464-514-1	Sequence 1, Appl1	939	20	0.7	2920	4	US-10-158-847-137	Sequence 137, App
867	20	0.7	2304	4	US-09-311-021-199	Sequence 199, App	940	20	0.7	2931	4	US-09-623-624-11	Sequence 1, Appl1
868	20	0.7	2311	4	US-09-665-479A-19	Sequence 19, Appl	941	20	0.7	2931	4	US-10-270-595-1	Sequence 1, Appl1
869	20	0.7	2315	1	US-08-333-358-13	Sequence 13, Appl	942	20	0.7	2935	4	US-09-636-215-333	Sequence 333, App
870	20	0.7	2315	1	US-08-663-694-13	Sequence 13, Appl	943	20	0.7	3001	4	US-09-539-333D-187	Sequence 187, App
871	20	0.7	2315	1	US-08-694-501-13	Sequence 13, Appl	944	20	0.7	3015	4	US-09-710-279-4306	Sequence 4306, Ap
872	20	0.7	2326	4	US-10-162-012-26	Sequence 26, Appl	945	20	0.7	3030	3	US-09-439-313-333	Sequence 333, App
873	20	0.7	2334	1	US-08-062-632-4	Sequence 4, Appl1	946	20	0.7	3030	3	US-09-352-616A-333	Sequence 333, App
874	20	0.7	2370	1	US-08-117-907-1	Sequence 1, Appl1	947	20	0.7	3030	4	US-09-232-149A-333	Sequence 333, App
875	20	0.7	2370	3	US-08-453-040-1	Sequence 1, Appl1	948	20	0.7	3030	4	US-09-636-215-333	Sequence 333, App
876	20	0.7	2372	3	US-09-145-391-1	Sequence 1, Appl1	949	20	0.7	3030	4	US-09-685-166A-333	Sequence 333, App
877	20	0.7	2372	3	US-09-794-591-1	Sequence 1, Appl1	950	20	0.7	3030	4	US-09-688-489-333	Sequence 333, App
878	20	0.7	2394	3	US-09-027-064-1	Sequence 1, Appl1	951	20	0.7	3030	4	US-09-679-426-333	Sequence 333, App
879	20	0.7	2394	3	US-09-371-815-1	Sequence 1, Appl1	952	20	0.7	3080	3	US-09-099-041A-35	Sequence 25, Appl
880	20	0.7	2395	4	US-09-270-767-11401	Sequence 11401, A	953	20	0.7	3080	3	US-09-245-281-25	Sequence 25, Appl
881	20	0.7	2400	6	5215909-13	Patent No. 5215909	954	20	0.7	3080	4	US-09-207-358B-25	Sequence 25, Appl
882	20	0.7	2406	1	US-08-396-479B-7	Sequence 7, Appl1	955	20	0.7	3080	4	US-09-340-620A-25	Sequence 25, Appl
883	20	0.7	2406	1	US-08-818-823-7	Sequence 7, Appl1	956	20	0.7	3080	4	US-09-865-364-25	Sequence 25, Appl
884	20	0.7	2424	3	US-09-234-393-1	Sequence 1, Appl1	957	20	0.7	3095	6	5231168-1	Patent No. 5231168
885	20	0.7	2424	4	US-09-360-545-15	Sequence 15, Appl	958	20	0.7	3107	3	US-08-213-419B-1	Sequence 1, Appl1
886	20	0.7	2424	4	US-09-865-171-1	Sequence 1, Appl1	959	20	0.7	3113	4	US-10-028-272-1	Sequence 1, Appl1
887	20	0.7	2424	4	US-09-398-395A-45	Sequence 45, Appl	960	20	0.7	3180	2	US-08-500-857A-9	Sequence 9, Appl1
888	20	0.7	2424	4	US-09-887-586A-45	Sequence 45, Appl	961	20	0.7	3191	3	US-08-675-816-3	Sequence 3, Appl1
889	20	0.7	2424	4	US-09-895-752-45	Sequence 45, Appl	962	20	0.7	3250	3	US-08-617-860B-1	Sequence 1, Appl1
890	20	0.7	2424	4	US-09-903-012B-45	Sequence 45, Appl	963	20	0.7	3252	3	US-09-118-442-1	Sequence 1, Appl1
891	20	0.7	2424	4	US-09-900-797-45	Sequence 45, Appl	964	20	0.7	3252	3	US-09-677-064-1	Sequence 1, Appl1
892	20	0.7	2445	6	5215909-9	Patent No. 5215909	965	20	0.7	3282	3	US-08-971-188-3	Sequence 3, Appl1
893	20	0.7	2458	3	US-08-611-587-6	Sequence 6, Appl1	966	20	0.7	3299	4	US-09-800-729-68	Sequence 68, Appl
894	20	0.7	2467	3	US-08-753-007A-1	Sequence 1, Appl1	967	20	0.7	3312	4	US-09-669-751-239	Sequence 239, App
895	20	0.7	2467	3	US-09-398-496-1	Sequence 1, Appl1	968	20	0.7	3337	2	US-08-072-610-1	Sequence 1, Appl1
896	20	0.7	2470	3	US-09-091-725-18	Sequence 18, Appl	969	20	0.7	3337	2	US-08-719-822B-1	Sequence 1, Appl1
897	20	0.7	2481	4	US-09-585-173B-11	Sequence 11, Appl	970	20	0.7	3337	4	US-09-092-45E-1	Sequence 1, Appl1
898	20	0.7	2483	2	US-08-177-109A-1	Sequence 1, Appl1	971	20	0.7	3337	4	US-08-719-822C-1	Sequence 1, Appl1
899	20	0.7	2483	2	US-08-687-706-1	Sequence 1, Appl1	972	20	0.7	3385	1	US-08-405-392-1	Sequence 1, Appl1
900	20	0.7	2488	4	US-09-816-093-1	Sequence 1, Appl1	973	20	0.7	3385	3	US-08-487-691-1	Sequence 1, Appl1
901	20	0.7	2500	4	US-08-426-509A-3	Sequence 3, Appl1	974	20	0.7	3385	3	US-08-666-221B-3	Sequence 3, Appl1
902	20	0.7	2500	4	US-08-232-545-3	Sequence 3, Appl1	975	20	0.7	3385	3	US-08-666-221B-9	Sequence 9, Appl1
903	20	0.7	2500	5	PCT-US95-05008-3	Sequence 3, Appl1	976	20	0.7	3385	4	US-08-189-738A-1	Sequence 1, Appl1

977 20 0.7 3454 4 US-09-270-767-11909
 c 978 20 0.7 3467 3 US-08-972-719-1
 c 979 20 0.7 3467 3 US-08-753-038-1
 c 980 20 0.7 3467 3 US-09-590-175-1
 981 20 0.7 3521 3 US-09-585-173B-35
 982 20 0.7 3532 3 US-08-787-739-90
 983 20 0.7 3532 3 US-09-178-115-90
 984 20 0.7 3532 3 US-09-177-776-90
 985 20 0.7 3604 4 US-09-801-191A-1
 986 20 0.7 3623 4 US-09-918-909A-23
 987 20 0.7 3637 1 US-08-445-640-3
 988 20 0.7 3637 3 US-08-170-558-3
 989 20 0.7 3637 3 US-08-447-314-3
 990 20 0.7 3637 3 US-08-445-461-3
 991 20 0.7 3674 4 US-09-482-273-73
 992 20 0.7 3740 4 US-09-489-847-14
 993 20 0.7 3745 4 US-09-270-767-9995
 994 20 0.7 3752 4 US-09-149-476-127
 995 20 0.7 3754 2 US-08-820-170A-12
 996 20 0.7 3754 3 US-09-055-699-12
 997 20 0.7 3754 3 US-09-273-565-12
 998 20 0.7 3754 3 US-09-565-538-12
 999 20 0.7 3754 3 US-09-661-468-12
 1000 20 0.7 3754 4 US-09-976-165-12

ALIGNMENTS

Sequence 11909, A
 Sequence 1, Appl1
 Sequence 1, Appl1
 Sequence 1, Appl1
 Sequence 35, Appl1
 Sequence 90, Appl1
 Sequence 90, Appl1
 Sequence 90, Appl1
 Sequence 90, Appl1
 Sequence 23, Appl1
 Sequence 23, Appl1
 Sequence 3, Appl1
 Sequence 3, Appl1
 Sequence 3, Appl1
 Sequence 3, Appl1
 Sequence 127, Appl1
 Sequence 12, Appl1
 Sequence 12, Appl1
 Sequence 12, Appl1
 Sequence 12, Appl1
 Sequence 12, Appl1

RESULT 1
 US-07-847-010-18/c
 ; Sequence 18, Application US/07847010
 ; Patent No. 5693495
 ; GENERAL INFORMATION:
 ; APPLICANT: Breiteneder, Heimo
 ; APPLICANT: Reikertorfer, Arnold
 ; APPLICANT: Valenta, Rudolf
 ; APPLICANT: Hoffmann - Sommergruber, Karin
 ; APPLICANT: Breitenbach, Michael
 ; APPLICANT: Kraft, Dietrich
 ; APPLICANT: Rumpold, Helmut
 ; APPLICANT: Scheiner, Otto
 ; APPLICANT: Ebner, Christof
 ; APPLICANT: Ferreira, Fatima
 ; TITLE OF INVENTION: Allergens of Alder Pollen and
 ; TITLE OF INVENTION: Applications Thereof
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER READABLE FORM:
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/847, 010
 ; FILING DATE: 01-JUN-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jones III, Harry C
 ; REGISTRATION NUMBER: 20, 280
 ; REFERENCE/DOCKET NUMBER: 6530-010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELE: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 860 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: hazel (Corylus sp.)
 ; IMMEDIATE SOURCE:
 ; LIBRARY: POLLEN FROM ALLERCON AB, ENGELHOLM, SWEDEN
 ; US-07-847-010-18

Query Match 1.0%; Score 26; DB 1; Length 860;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 26; Conservative 0; Indels 0; Gaps 0;

Qy 2654 AATTGACAAAAA 2679
 Db 754 AATTGACAAAAA 729

RESULT 2
 US-09-522-714-15
 ; Sequence 15, Application US/09522714
 ; Patent No. 6563020
 ; GENERAL INFORMATION:
 ; APPLICANT: Simmons, Carl R.
 ; APPLICANT: Yalpani, Nasser
 ; TITLE OF INVENTION: Maize Chitinases and Their Use in
 ; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
 ; FILE REFERENCE: 1100
 ; CURRENT APPLICATION NUMBER: US/09/522, 714
 ; CURRENT FILING DATE: 2000-03-10
 ; EARLIER APPLICATION NUMBER: 60/125, 915
 ; EARLIER FILING DATE: 1999-03-24
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 1085
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (46)...(966)
 ; US-09-522-714-15

Query Match 0.9%; Score 25; DB 4; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2655 AATTGACAAAAA 2679
 Db 1061 AATTGACAAAAA 1085

RESULT 3
 US-09-248-796A-11988
 ; Sequence 11988, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248, 796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074, 725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096, 409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 11988

LENGTH: 258
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-11988

Query Match 0.9%; Score 24; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 220 ATTGACAAAAA 243

RESULT 4
5198347-3
Patent No. 5198347
APPLICANT: MILLER, LOUIS H.; ADAMS, JOHN H.; KASLOW,
DAVIC C.; FANG, XIANGDOUG
TITLE OF INVENTION: DNA ENCODING PLASMIDIUM VIVAX AND
PLASMIDIUM KNOWLES DUFFY RECEPTOR
NUMBER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,837
FILING DATE: 20-JUL-1990
SEQ ID NO: 3
LENGTH: 3157
5198347-3

Query Match 0.9%; Score 24; DB 6; Length 3157;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 3088 ATTGACAAAAA 3111

RESULT 5
US-09-621-976-17572
Sequence 17572, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17572
LENGTH: 443
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17572

Query Match 0.9%; Score 23; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAA 2679
DB 420 TTGACAAAAA 442

RESULT 6
US-09-614-912-161
Sequence 161, Application US/09614912
Patent No. 6677502
GENERAL INFORMATION:
APPLICANT: Allen, Steve

APPLICANT: Rafalski, Antoni
APPLICANT: Orozco, Buddy
APPLICANT: Miao, Gou-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BE1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 161
LENGTH: 1185
TYPE: DNA
ORGANISM: Glycine max
US-09-614-912-161

Query Match 0.9%; Score 23; DB 4; Length 1185;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAA 2679
DB 1163 TTGACAAAAA 1185

RESULT 7
US-09-412-102-1
Sequence 1, Application US/09412102
Patent No. 622892
GENERAL INFORMATION:
APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY B
TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
TITLE OF INVENTION: NEMATODES IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,102
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/217,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-18P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Zea mays
IMMEDIATE SOURCE:
CLONE: P12217
FEATURE:
NAME/KEY: CDS
LOCATION: 146..994
US-09-412-102-1

Query Match 0.9%; Score 23; DB 3; Length 1347;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAA 2679
DB 1325 TTGACAAAAAAAAAAAAAAAAA 1347

RESULT 8
US-09-217-787-1
Sequence 1, Application US/09217787
Patent No. 6284948
GENERAL INFORMATION:
APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E
TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
TITLE OF INVENTION: NEMATODES IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,787
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-18P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Zea mays
IMMEDIATE SOURCE:

CLONE: P12217
FEATURE:
NAME/KEY: CDS
LOCATION: 146..994
US-09-217-787-1

Query Match 0.9%; Score 23; DB 3; Length 1347;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAA 2679
DB 1325 TTGACAAAAAAAAAAAAAAAAA 1347

RESULT 9
US-08-484-101B-35
Sequence 35, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: ETHYLENE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Treccartin
STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2405 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 288..2196
US-08-484-101B-35

Query Match 0.9%; Score 23; DB 1; Length 2405;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAA 2679
DB 2378 TTGACAAAAAAAAAAAAAAAAA 2400

RESULT 10
US-08-484-101B-49
; Sequence 49, Application US/08484101B
; Patent No. 5824868
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Treacartin
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,101B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,555
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 288..2196
US-08-484-101B-49

Query Match 0.9%; Score 23; DB 1; Length 2405;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 2378 TTGACAAAAAAAAAAAAAAAAAAAA 2400

RESULT 11
US-08-714-524D-35
; Sequence 35, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Bleecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D

; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 35
; LENGTH: 2405
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (288)..(2195)
US-08-714-524D-35

Query Match 0.9%; Score 23; DB 3; Length 2405;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 2378 TTGACAAAAAAAAAAAAAAAAAAAA 2400

RESULT 12
US-08-714-524D-49
; Sequence 49, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Bleecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 49
; LENGTH: 2405
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (288)..(2195)
US-08-714-524D-49

Query Match 0.9%; Score 23; DB 3; Length 2405;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 2378 TTGACAAAAAAAAAAAAAAAAAAAA 2400

RESULT 13
US-09-270-767-8213
; Sequence 8213, Application US/09270767
; Patent No. 6703451
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 8213
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8213

Query Match 0.8%; Score 22; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 93 TGACAAAAA 114

RESULT 14

US-09-270-767-23495
Sequence 23495, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23495
LENGTH: 121
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-23495

Query Match 0.8%; Score 22; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679

Db 93 TGACAAAAA 114

RESULT 15

US-08-244-113-18
Sequence 18, Application US/08244113
Patent No. 5455181
GENERAL INFORMATION:
APPLICANT: Strube, Karl-Hermann
APPLICANT: Bialojan, Siegfried
APPLICANT: Kroege, Burkhard
APPLICANT: Friedrich, Thomas
TITLE OF INVENTION: No. 5455181el thrombin-inhibitory proteins from terrestrial
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauff
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,113
FILING DATE:

CLASSIFICATION: 530
CLASSIFICATION: C07K 73/10
CLASSIFICATION: A61K 37/64
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP92/02661
FILING DATE: 19-NOV-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-244-113-18

Query Match 0.8%; Score 22; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 224 TGACAAAAA 245

RESULT 16

US-09-280-116-159/C
Sequence 159, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 159
LENGTH: 424
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Lon family of ATP-dependent proteases
US-09-280-116-159

Query Match 0.8%; Score 22; DB 3; Length 424;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679

Db 22 TGACAAAAA 1

RESULT 17

US-09-311-021-161
Sequence 161, Application US/09311021
Patent No. 6706869
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agoetino, Michael J.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
CURRENT APPLICATION NUMBER: US/09/311,021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 161
LENGTH: 622
TYPE: DNA
ORGANISM: Homo sapiens
US-09-311-021-161

Query Match 0.8%; Score 22; DB 4; Length 622;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 589 TGACAAAAA 610

RESULT 18

US-09-205-258-172

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/ Sequence 172, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P1
/ CURRENT FILING DATE: US/09/205,258
/ EARLIER APPLICATION NUMBER: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,882
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,899
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,900
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,901
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,892
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,915
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,019
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,970
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,972
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,916
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,373
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,875
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,374
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,917
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,949
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,883
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,897
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,898
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/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,962
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 172
/ LENGTH: 786
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-205-258-172

Query Match          0.8%; Score 22; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2658 TGACCAAAAAAAAAAAAAA 2679
Db      760 TGACCAAAAAAAAAAAAAA 781

RESULT 19
US-09-270-767-5937
/ Sequence 5937, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT FILING DATE: US/09/270,767
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 5937
/ LENGTH: 809
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
US-09-270-767-5937

Query Match          0.8%; Score 22; DB 4; Length 809;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2658 TGACCAAAAAAAAAAAAAA 2679
Db      787 TGACCAAAAAAAAAAAAAA 808

RESULT 20
US-09-270-767-21219
/ Sequence 21219, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT FILING DATE: US/09/270,767
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 21219
/ LENGTH: 809
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-21219

Query Match      0.8%; Score 22; DB 4; Length 809;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2658 TGCACAAAAAAAAAAAAAAAAA 2679
Db      787 TGCACAAAAAAAAAAAAAAAAA 808

RESULT 21
US-09-205-258-190/c
; Sequence 190, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,173
; EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 190
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-205-258-190

Query Match      0.8%; Score 22; DB 4; Length 906;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2657 TTGACAAAAAAAAAAAAAAAAA 2678
Db      843 TTGACAAAAAAAAAAAAAAAAA 822

RESULT 22
US-09-475-316A-24
; Sequence 24, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINO/LARICRESTINOL REDUCTASES
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
; FILE REFERENCE: WSUR-1-13793
; CURRENT FILING DATE: US/09/475,316A
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653

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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 914
TYPE: DNA
ORGANISM: *Thuja plicata*
FEATURE:
NAME/KEY: CDS
LOCATION: (94)..(669)
US-09-475-316A-24

Query Match
Best Local Similarity 100.0%; Score 22; DB 3; Length 914;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAA 2678
DB 893 TTGACAAAAAAAAAAAAAAAAA 914

RESULT 23
US-09-704-640-24
Sequence 24, Application US/09704640
Patent No. 6635459
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6635459man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINOCESINOL/LARICRESINOL REDUCTASE,
FILE REFERENCE: MSUR-1-16492
CURRENT APPLICATION NUMBER: US/09/704,640
CURRENT FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 09/475,316
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/307,653
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 914
TYPE: DNA
ORGANISM: *Thuja plicata*
FEATURE:
NAME/KEY: CDS
LOCATION: (94)..(669)
US-09-704-640-24

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 914;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAAA 2678
DB 893 TTGACAAAAAAAAAAAAAAAAA 914

RESULT 24
US-09-183-861-19
Sequence 19, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/183,861
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: *Leishmania major*
FEATURE:
NAME/KEY: CDS
LOCATION: 71..523
US-09-183-861-19

Query Match
Best Local Similarity 100.0%; Score 22; DB 3; Length 1019;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAAAAAAAAAAAAAA 2679
DB 991 TGACAAAAAAAAAAAAAAAAA 1012

RESULT 25
US-09-022-765-19
Sequence 19, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND

NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
FAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Leishmania major
FEATURE:
NAME/KEY: CDS
LOCATION: 71..523
US-09-022-765-19

Query Match 0.8%; Score 22; DB 3; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACCAAAAAAAAAAAAAAAAAA 2679
|||||
DB 991 TGACCAAAAAAAAAAAAAAAAAA 1012

RESULT 26
US-09-551-974A-19
Sequence 19, Application US/09551974A
Patent No. 6500437
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
US-09-551-974A-19

Query Match 0.8%; Score 22; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACCAAAAAAAAAAAAAAAAAA 2679
|||||
DB 991 TGACCAAAAAAAAAAAAAAAAAA 1012

RESULT 27
US-09-565-501A-19
Sequence 19, Application US/09565501A
Patent No. 6607731
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Peter Probst
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
US-09-565-501A-19

Query Match 0.8%; Score 22; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACCAAAAAAAAAAAAAAAAAA 2679
|||||
DB 991 TGACCAAAAAAAAAAAAAAAAAA 1012

RESULT 28
US-09-639-206A-19
Sequence 19, Application US/09639206A
Patent No. 6613337
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C7
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
US-09-639-206A-19

Query Match 0.8%; Score 22; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACCAAAAAAAAAAAAAAAAAA 2679
|||||

Db 991 TGACAAAAA 1012

RESULT 29
US-09-874-923-19
Sequence 19, Application US/09874923
Patent No. 6638517
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasser A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
US-09-874-923-19

Query Match 0.8%; Score 22; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 991 TGACAAAAA 1012

RESULT 30
US-08-798-841-19
Sequence 19, Application US/08798841
Patent No. 6709661
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,841
FILING DATE: 12-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Leishmania major
FEATURE:
NAME/KEY: CDS
LOCATION: 71..523
US-08-798-841-19

Query Match 0.8%; Score 22; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 991 TGACAAAAA 1012

RESULT 31
US-09-232-200-50
Sequence 50, Application US/09232200A
Patent No. 6288213
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-232-200-50

Query Match 0.8%; Score 22; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
Db 1140 TGACAAAAA 1161

RESULT 32
US-09-232-197-50
Sequence 50, Application US/09232197A
Patent No. 6300096
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374

EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-232-197-50

Query Match 0.8%; Score 22; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAAAAAAAAAAAAAAAAA 2679
DB 1140 TGACAAAAAAAAAAAAAAAAAAAA 1161

RESULT 33

US-09-232-201-50
Sequence 50, Application US/09232201A
Patent No. 6348321
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21P3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
EARLIER FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-232-201-50

Query Match 0.8%; Score 22; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAAAAAAAAAAAAAAAAA 2679
DB 1140 TGACAAAAAAAAAAAAAAAAAAAA 1161

RESULT 34

US-09-232-195-50
Sequence 50, Application US/09232195A
Patent No. 6657049
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21P3MD
CURRENT APPLICATION NUMBER: US/09/232,195A
CURRENT FILING DATE: 1999-01-04

EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-232-195-50

Query Match 0.8%; Score 22; DB 4; Length 1173;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAAAAAAAAAAAAAAAAA 2679
DB 1140 TGACAAAAAAAAAAAAAAAAAAAA 1161

RESULT 35

US-09-064-411A-35
Sequence 35, Application US/09064411A
Patent No. 6331664
GENERAL INFORMATION:
APPLICANT: Rubin-Wilson, Beth
APPLICANT: Guo, Liming
APPLICANT: Skokut, Tom
APPLICANT: Young, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Armstrong, Katherine
APPLICANT: Cowen, Neil M.
TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP
TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and
TITLE OF INVENTION: Their Use in the Regulation of Fatty Acid Content of Oil
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agrosciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,411A
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,827
FILING DATE: 05-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: CDS
LOCATION: 38..1135
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 140..1135
US-09-064-411A-35

Query Match 0.8%; Score 22; DB 3; Length 1287;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TTGACAAAAA 2679
DB 1265 TTGACAAAAA 1286

RESULT 36
US-08-979-608A-10
Sequence 10, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
Lees, Robert S.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-Mar-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELEPHONE: 617/542-8906

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 10:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 58..510

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-979-608A-10

Query Match 0.8%; Score 22; DB 3; Length 1404;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAA 2678

DB 1383 TTGACAAAAA 1404

RESULT 37
US-09-517-849-10
Sequence 10, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
Lees, Robert S.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-003001

TELEPHONE: 617/542-8906

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 10:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 58..510

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-517-849-10

Query Match 0.8%; Score 22; DB 4; Length 1404;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAA 2678

DB 1383 TTGACAAAAA 1404

RESULT 38
US-09-616-289-10
Sequence 10, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
Lees, Robert S.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110-2804

```

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58) ... (510)
US-09-616-289-10

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 1404;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2657 TTGACAAAAAAAAAAAAAAAAA 2678
Db 1383 TTGACAAAAAAAAAAAAAAAAA 1404

RESULT 39
US-09-347-650-15
; Sequence 15, Application US/09347650
; Patent No. 6576814
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven
; TITLE OF INVENTION: Manipulation of M10 Genes to Enhance Disease Resistance
; FILE REFERENCE: 5718-42035718/158714
; CURRENT APPLICATION NUMBER: US/09/347,650
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: M109
US-09-347-650-15

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 1557;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2658 TGACAAAAAAAAAAAAAAAAA 2679
Db 1531 TGACAAAAAAAAAAAAAAAAA 1552

RESULT 40
US-09-268-140-11
; Sequence 11, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
```

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; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-268-140-11

Query Match
Best Local Similarity 100.0%; Score 22; DB 3; Length 2339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2658 TGACAAAAAAAAAAAAAAAAA 2679
Db 2317 TGACAAAAAAAAAAAAAAAAA 2338

RESULT 41
US-07-867-106-5/c
; Sequence 5, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELEPHONE: 215-568-1100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2422 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
US-07-867-106-5

Query Match
Best Local Similarity 100.0%; Score 22; DB 1; Length 2422;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2658 TGACAAAAAAAAAAAAAAAAA 2679
```

DB 2295 TGACAAAAA 2274

RESULT 42

US-09-268-140-1
Sequence 1, Application US/09268140
Patent No. 6268176
GENERAL INFORMATION:
APPLICANT: Gemmell, Robert M.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2505
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (238) ..(2232)
US-09-268-140-1

Query Match

Best Local Similarity 0.8%; Score 22; DB 3; Length 2505;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679

DB 2483 TGACAAAAA 2504

RESULT 43

US-09-268-140-7
Sequence 7, Application US/09268140
Patent No. 6268176
GENERAL INFORMATION:
APPLICANT: Gemmell, Robert M.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 2517
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: repeat unit
LOCATION: (165) ..(176)
US-09-268-140-7

Query Match

Best Local Similarity 0.8%; Score 22; DB 3; Length 2517;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679

DB 2495 TGACAAAAA 2516

RESULT 44

US-09-604-605-1
Sequence 1, Application US/09604605
Patent No. 6421613

GENERAL INFORMATION:

APPLICANT: Ramgopal Nadiampalli
APPLICANT: Carl R. Simons
TITLE OF INVENTION: Maize Prolifera Gene and Uses Thereof
FILE REFERENCE: 1138
CURRENT APPLICATION NUMBER: US/09/604,605
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/143,222
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2533
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (110) ..(2269)
US-09-604-605-1

Query Match

Best Local Similarity 0.8%; Score 22; DB 4; Length 2533;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679

DB 2509 TGACAAAAA 2530

RESULT 45

US-08-160-861-1
Sequence 1, Application US/08160861
Patent No. 5539295
GENERAL INFORMATION:
APPLICANT: MORRIS, STEPHAN W
TITLE OF INVENTION: NOVEL FUSION NUCLEIC ACID SEQUENCES AND
TITLE OF INVENTION: FUSION PROTEINS PRESENT IN HUMAN t(2;5) LYMPHOMA, METHODS
TITLE OF INVENTION: OF DETECTION AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVE NW SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,861
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36217
REFERENCE/DOCKET NUMBER: 0656.0400000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2608 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1719
US-08-160-861-1

Query Match

0.8%; Score 22; DB 1; Length 2608;

Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
DB 2585 TGACAAAAA 2606

RESULT 46

US-10-140-002-345
Sequence 345, Application US/10140002
Patent No. 6725730

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 345
LENGTH: 2933
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-345

Query Match 0.8%; Score 22; DB 4; Length 2933;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
DB 2872 TGACAAAAA 2893

RESULT 47

US-07-867-106-4/C
Sequence 4, Application US/07867106
Patent No. 5389526

GENERAL INFORMATION:

APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3138 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-07-867-106-4

Query Match 0.8%; Score 22; DB 1; Length 3138;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGACAAAAA 2679
DB 3011 TGACAAAAA 2990

RESULT 48

US-07-867-106-2
Sequence 2, Application US/07867106
Patent No. 5389526

GENERAL INFORMATION:

APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2378..5038
NAME/KEY: CDS
LOCATION: 2378..5038
US-07-867-106-2

Query Match 0.8%; Score 22; DB 1; Length 5852;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGCACAAAAA 2679
DB 943 TGCACAAAAA 964

RESULT 49
US-07-867-106-2/c
Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Peeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2378..5038
FEATURE:

NAME/KEY: CDS
LOCATION: 2378..5038
US-07-867-106-2

Query Match 0.8%; Score 22; DB 1; Length 5852;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2658 TGCACAAAAA 2679
DB 1647 TGCACAAAAA 1626

RESULT 50
US-08-836-022A-10
Sequence 10, Application US/08836022A
Patent No. 6001557
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-836-022A-10

Query Match 0.8%; Score 22; DB 3; Length 19307;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAA 2678
DB 14579 TTGACAAAAA 14600

Search completed: January 15, 2005, 12:28:41
Job time : 253 secs

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C 89	23	0.9	842	16	US-10-425-114-29088	Sequence 29088, A	162	22	0.8	193	16	US-10-242-5354-47068	Sequence 47068, A
C 90	23	0.9	853	18	US-10-425-115-25688	Sequence 25688, A	163	22	0.8	193	16	US-10-085-783A-47068	Sequence 47068, A
C 91	23	0.9	878	18	US-10-739-930-139	Sequence 139, App	164	22	0.8	205	9	US-09-925-299-617	Sequence 617, App
C 92	23	0.9	884	18	US-10-425-115-118822	Sequence 118822, A	165	22	0.8	205	10	US-09-925-299-617	Sequence 617, App
C 93	23	0.9	922	15	US-10-017-161-1121	Sequence 1121, App	166	22	0.8	220	16	US-10-242-5354-53590	Sequence 53590, A
C 94	23	0.9	922	15	US-10-292-798-949	Sequence 949, App	167	22	0.8	220	16	US-10-085-783A-53590	Sequence 53590, A
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C 96	23	0.9	963	11	US-09-764-875-114	Sequence 114, App	169	22	0.8	223	16	US-10-085-783A-47151	Sequence 47151, A
C 97	23	0.9	966	18	US-10-425-115-93727	Sequence 93727, A	170	22	0.8	225	17	US-10-767-701-29167	Sequence 29167, A
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C 99	23	0.9	980	18	US-10-425-115-49081	Sequence 49081, App	172	22	0.8	237	16	US-10-242-5354-45421	Sequence 45421, A
C 100	23	0.9	1026	17	US-10-767-701-12139	Sequence 12139, A	173	22	0.8	237	16	US-10-085-783A-45421	Sequence 45421, A
C 101	23	0.9	1113	16	US-10-424-599-70311	Sequence 70311, A	174	22	0.8	239	10	US-09-814-553-5550	Sequence 5550, App
C 102	23	0.9	1125	9	US-09-770-445-86	Sequence 86, App1	175	22	0.8	259	18	US-09-814-553-5550	Sequence 11837, A
C 103	23	0.9	1181	18	US-10-425-115-63246	Sequence 63246, A	176	22	0.8	259	18	US-10-425-115-53114	Sequence 53114, A
C 104	23	0.9	1234	18	US-10-739-930-662	Sequence 662, App	177	22	0.8	267	18	US-10-425-115-136548	Sequence 136548, A
C 105	23	0.9	1262	17	US-10-437-963-22316	Sequence 22316, A	178	22	0.8	275	9	US-09-960-352-4469	Sequence 4469, App
C 106	23	0.9	1263	9	US-09-361-630-11	Sequence 11, App1	179	22	0.8	282	18	US-10-425-115-163390	Sequence 163390, A
C 107	23	0.9	1278	11	US-09-939-853A-18	Sequence 18, App1	180	22	0.8	303	18	US-10-425-115-74113	Sequence 74113, A
C 108	23	0.9	1278	11	US-09-939-853A-20	Sequence 20, App1	181	22	0.8	322	17	US-10-437-963-90190	Sequence 90190, A
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C 110	23	0.9	1299	17	US-10-437-963-81025	Sequence 81025, A	183	22	0.8	330	10	US-09-803-719-1704	Sequence 1704, App
C 111	23	0.9	1337	18	US-10-425-115-61928	Sequence 61928, A	184	22	0.8	330	14	US-10-040-862-5382	Sequence 5382, App
C 112	23	0.9	1424	17	US-10-767-701-13472	Sequence 13472, A	185	22	0.8	330	16	US-10-057-475B-5382	Sequence 5382, App
C 113	23	0.9	1449	18	US-10-425-115-161556	Sequence 161556, A	186	22	0.8	330	16	US-10-154-884B-5382	Sequence 5382, App
C 114	23	0.9	1537	18	US-10-357-930-25070	Sequence 25070, A	187	22	0.8	330	17	US-10-764-324-5382	Sequence 5382, App
C 115	23	0.9	1642	18	US-10-425-115-102900	Sequence 102900, A	188	22	0.8	332	16	US-10-424-599-256	Sequence 256, App
C 116	23	0.9	1643	17	US-10-437-963-33720	Sequence 33720, A	189	22	0.8	349	18	US-10-425-115-170460	Sequence 170460, A
C 117	23	0.9	1674	18	US-10-425-115-53306	Sequence 53306, A	190	22	0.8	351	16	US-10-424-599-35031	Sequence 35031, A
C 118	23	0.9	1808	18	US-10-425-115-132423	Sequence 132423, A	191	22	0.8	352	10	US-09-814-553-18021	Sequence 18021, A
C 119	23	0.9	1811	17	US-10-437-963-90919	Sequence 90919, A	192	22	0.8	359	9	US-09-770-791-557	Sequence 557, App
C 120	23	0.9	1857	17	US-10-425-115-11692	Sequence 11692, A	193	22	0.8	366	18	US-10-425-115-148883	Sequence 148883, A
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C 122	23	0.9	2000	9	US-09-887-576-151	Sequence 151, App	195	22	0.8	368	16	US-10-085-783A-15575	Sequence 15575, A
C 123	23	0.9	2000	9	US-09-938-842A-2723	Sequence 2723, App	196	22	0.8	376	18	US-10-357-930-1364	Sequence 1364, A
C 124	23	0.9	2000	9	US-09-938-842A-3091	Sequence 3091, App	197	22	0.8	380	9	US-09-964-824A-1335	Sequence 344, App
C 125	23	0.9	2000	9	US-09-938-842A-5117	Sequence 5117, App	198	22	0.8	380	9	US-09-880-107-4661	Sequence 1135, App
C 126	23	0.9	2000	11	US-09-938-842A-2723	Sequence 2723, App	199	22	0.8	385	18	US-10-425-115-152116	Sequence 152116, A
C 127	23	0.9	2000	11	US-09-938-842A-3091	Sequence 3091, App	200	22	0.8	396	10	US-09-910-082A-1318	Sequence 138, App
C 128	23	0.9	2000	11	US-09-938-842A-5117	Sequence 5117, App	201	22	0.8	396	17	US-10-765-826-1038	Sequence 1038, App
C 129	23	0.9	2038	18	US-10-425-115-68300	Sequence 68300, A	202	22	0.8	398	16	US-10-424-599-101855	Sequence 101855, A
C 130	23	0.9	2095	16	US-10-424-599-68226	Sequence 68226, A	203	22	0.8	402	16	US-10-424-599-41097	Sequence 41097, A
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C 132	23	0.9	2253	17	US-10-437-963-34768	Sequence 34768, A	205	22	0.8	415	16	US-10-242-535A-16610	Sequence 16610, A
C 133	23	0.9	2508	18	US-10-425-115-9789	Sequence 9789, App	206	22	0.8	418	17	US-10-085-783A-16610	Sequence 16610, A
C 134	23	0.9	2582	9	US-09-839-185-7	Sequence 7, App1	207	22	0.8	418	17	US-10-437-963-9142	Sequence 9142, App
C 135	23	0.9	2753	9	US-09-789-561-15	Sequence 15, App1	208	22	0.8	420	16	US-10-424-599-40888	Sequence 40888, A
C 136	23	0.9	2878	16	US-10-424-599-55254	Sequence 55254, A	209	22	0.8	421	9	US-09-880-107-4661	Sequence 3661, App
C 137	23	0.9	2910	16	US-10-001-885-40	Sequence 40, App1	210	22	0.8	423	9	US-09-960-352-8869	Sequence 8869, App
C 138	23	0.9	2950	13	US-10-027-632-250028	Sequence 250028, A	211	22	0.8	423	10	US-09-918-995-4093	Sequence 4093, App
C 139	23	0.9	2950	13	US-10-027-632-250030	Sequence 250030, A	212	22	0.8	423	14	US-10-066-543-2994	Sequence 2994, App
C 140	23	0.9	2950	13	US-10-027-632-250031	Sequence 250031, A	213	22	0.8	428	18	US-10-425-115-40957	Sequence 40957, A
C 141	23	0.9	2950	15	US-10-027-632-250028	Sequence 250028, A	214	22	0.8	428	18	US-10-357-930-34775	Sequence 34775, A
C 142	23	0.9	2950	15	US-10-027-632-250030	Sequence 250030, A	215	22	0.8	433	15	US-10-058-053A-76	Sequence 76, App1
C 143	23	0.9	2950	15	US-10-027-632-250031	Sequence 250031, A	216	22	0.8	433	17	US-10-838-226-76	Sequence 76, App1
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C 146	23	0.9	5243	16	US-10-399-225-17	Sequence 17, App1	219	22	0.8	443	16	US-10-621-901-1499	Sequence 1499, App
C 147	23	0.9	5397	17	US-10-755-889-105	Sequence 105, App	220	22	0.8	450	18	US-10-425-115-134817	Sequence 134817, A
C 148	23	0.9	5900	13	US-10-027-632-250029	Sequence 250029, A	221	22	0.8	472	17	US-10-437-963-13703	Sequence 13703, A
C 149	23	0.9	5900	15	US-10-027-632-250029	Sequence 250029, A	222	22	0.8	475	16	US-10-424-599-53675	Sequence 53675, A
C 150	23	0.9	8800	16	US-10-381-441-3	Sequence 3, App1	223	22	0.8	478	18	US-10-425-115-43811	Sequence 43811, A
C 151	23	0.9	28486	15	US-10-004-113-35	Sequence 25, App1	224	22	0.8	478	10	US-09-918-995-25488	Sequence 25488, A
C 152	23	0.9	28486	16	US-10-394-948-13	Sequence 13, App1	225	22	0.8	480	13	US-10-027-632-90331	Sequence 90331, A
C 153	23	0.9	52256	13	US-10-087-192-1399	Sequence 1399, App	226	22	0.8	480	15	US-10-027-632-90331	Sequence 90331, A
C 154	23	0.9	80374	16	US-10-041-018-376	Sequence 376, App	227	22	0.8	481	18	US-10-425-115-79711	Sequence 79711, A
C 155	23	0.9	158980	18	US-10-422-522-32	Sequence 32, App1	228	22	0.8	486	10	US-09-918-995-21449	Sequence 21449, A
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C 158	23	0.9	398287	17	US-10-741-601-5719	Sequence 5719, App	231	22	0.8	503	10	US-09-770-961-366	Sequence 366, App

C 232	22	0.8	507	17	US-10-437-963-86146	Sequence 86146, A	305	22	0.8	770	15	US-10-027-632-148328	Sequence 148328,
C 233	22	0.8	519	18	US-10-357-930-54035	Sequence 54035, A	C 306	22	0.8	773	13	US-10-027-632-33830	Sequence 33830, A
C 234	22	0.8	520	13	US-10-027-632-186676	Sequence 186676, A	C 307	22	0.8	773	15	US-10-027-632-13830	Sequence 13830, A
C 235	22	0.8	520	15	US-10-027-632-186676	Sequence 186676, A	C 308	22	0.8	779	10	US-09-764-891-9550	Sequence 9550, A
C 236	22	0.8	520	17	US-10-437-963-44476	Sequence 44476, A	C 309	22	0.8	779	15	US-10-205-428-878	Sequence 878, A
C 237	22	0.8	533	13	US-10-027-632-280202	Sequence 280202, A	C 310	22	0.8	782	10	US-09-764-891-9553	Sequence 9553, A
C 238	22	0.8	533	15	US-10-027-632-280202	Sequence 280202, A	C 311	22	0.8	782	15	US-10-205-428-881	Sequence 881, A
C 239	22	0.8	535	18	US-10-425-115-9699	Sequence 9699, A	C 312	22	0.8	785	18	US-10-425-115-52098	Sequence 52098, A
C 240	22	0.8	536	16	US-10-243-535A-14178	Sequence 14178, A	C 313	22	0.8	786	10	US-09-933-767-172	Sequence 172, A
C 241	22	0.8	536	16	US-10-085-783A-14178	Sequence 14178, A	C 314	22	0.8	786	14	US-10-004-860-172	Sequence 172, A
C 242	22	0.8	539	10	US-09-814-353-17047	Sequence 17047, A	C 315	22	0.8	786	14	US-10-023-282-172	Sequence 220, A
C 243	22	0.8	548	15	US-10-029-386-532	Sequence 532, A	C 316	22	0.8	832	9	US-09-925-299-220	Sequence 220, A
C 244	22	0.8	559	10	US-09-774-633-38	Sequence 38, A	C 317	22	0.8	832	14	US-10-102-806-220	Sequence 190, A
C 245	22	0.8	559	10	US-09-969-730-83	Sequence 83, A	C 318	22	0.8	862	18	US-10-425-115-171408	Sequence 171408, A
C 246	22	0.8	559	16	US-10-621-363-83	Sequence 83, A	C 319	22	0.8	881	14	US-10-198-846-5540	Sequence 5540, A
C 247	22	0.8	560	18	US-10-735-930-3846	Sequence 3846, A	C 320	22	0.8	889	14	US-10-198-846-6287	Sequence 6287, A
C 248	22	0.8	567	9	US-09-777-564-739	Sequence 739, A	C 321	22	0.8	906	10	US-09-933-767-190	Sequence 190, A
C 249	22	0.8	567	14	US-10-015-219-739	Sequence 739, A	C 322	22	0.8	906	14	US-10-004-860-190	Sequence 190, A
C 250	22	0.8	576	18	US-10-425-115-143483	Sequence 143483, A	C 323	22	0.8	906	14	US-10-023-282-190	Sequence 190, A
C 251	22	0.8	576	13	US-10-027-632-256677	Sequence 256677, A	C 324	22	0.8	928	18	US-10-425-115-122600	Sequence 122600, A
C 252	22	0.8	576	13	US-10-027-632-256678	Sequence 256678, A	C 325	22	0.8	928	18	US-10-425-115-122600	Sequence 122600, A
C 253	22	0.8	576	15	US-10-027-632-256677	Sequence 256677, A	C 326	22	0.8	958	17	US-10-437-963-15821	Sequence 15821, A
C 254	22	0.8	576	15	US-10-027-632-256678	Sequence 256678, A	C 327	22	0.8	966	18	US-10-425-115-98332	Sequence 98332, A
C 255	22	0.8	580	18	US-10-357-930-58036	Sequence 58036, A	C 328	22	0.8	976	18	US-10-723-860-7085	Sequence 7085, A
C 256	22	0.8	591	16	US-10-424-599-63033	Sequence 63033, A	C 329	22	0.8	990	15	US-10-411-224-58	Sequence 58, A
C 257	22	0.8	604	13	US-10-027-632-862	Sequence 862, A	C 330	22	0.8	990	16	US-10-047-021-58	Sequence 58, A
C 258	22	0.8	604	15	US-10-027-632-862	Sequence 862, A	C 331	22	0.8	1001	9	US-09-789-054A-23	Sequence 23, A
C 259	22	0.8	606	13	US-10-027-632-306532	Sequence 306532, A	C 332	22	0.8	1001	17	US-10-628-969-23	Sequence 23, A
C 260	22	0.8	606	15	US-10-027-632-306532	Sequence 306532, A	C 333	22	0.8	1005	18	US-10-739-930-2305	Sequence 2305, A
C 261	22	0.8	607	13	US-10-027-632-306509	Sequence 306509, A	C 334	22	0.8	1012	13	US-10-027-632-100959	Sequence 100959, A
C 262	22	0.8	607	13	US-10-027-632-306236	Sequence 306236, A	C 335	22	0.8	1012	13	US-10-027-632-100960	Sequence 100960, A
C 263	22	0.8	607	15	US-10-027-632-96509	Sequence 96509, A	C 336	22	0.8	1012	15	US-10-027-632-100959	Sequence 100959, A
C 264	22	0.8	607	15	US-10-027-632-306236	Sequence 306236, A	C 337	22	0.8	1012	15	US-10-027-632-100960	Sequence 100960, A
C 265	22	0.8	611	13	US-10-027-632-35090	Sequence 35090, A	C 338	22	0.8	1019	9	US-09-874-923-19	Sequence 19, A
C 266	22	0.8	611	15	US-10-027-632-35090	Sequence 35090, A	C 339	22	0.8	1019	9	US-09-991-496-19	Sequence 19, A
C 267	22	0.8	611	17	US-10-767-701-12972	Sequence 12972, A	C 340	22	0.8	1023	17	US-10-437-963-96859	Sequence 96859, A
C 268	22	0.8	612	13	US-10-027-632-15552	Sequence 15552, A	C 341	22	0.8	1033	18	US-10-425-115-6041	Sequence 6041, A
C 269	22	0.8	612	15	US-10-027-632-15552	Sequence 15552, A	C 342	22	0.8	1046	17	US-10-437-963-86584	Sequence 86584, A
C 270	22	0.8	616	10	US-09-814-353-2716	Sequence 2716, A	C 343	22	0.8	1062	17	US-10-437-963-20169	Sequence 20169, A
C 271	22	0.8	616	10	US-09-814-353-9049	Sequence 9049, A	C 344	22	0.8	1092	18	US-10-425-115-76006	Sequence 76006, A
C 272	22	0.8	627	11	US-09-969-034-1170	Sequence 1170, A	C 345	22	0.8	1096	18	US-10-425-115-40839	Sequence 40839, A
C 273	22	0.8	637	13	US-10-027-632-200439	Sequence 200439, A	C 346	22	0.8	1107	16	US-10-739-930-182	Sequence 182, A
C 274	22	0.8	637	13	US-10-027-632-296428	Sequence 296428, A	C 347	22	0.8	1107	16	US-10-424-599-15922	Sequence 15922, A
C 275	22	0.8	637	15	US-10-027-632-200439	Sequence 200439, A	C 348	22	0.8	1114	10	US-09-946-374-110	Sequence 110, A
C 276	22	0.8	637	15	US-10-027-632-296428	Sequence 296428, A	C 349	22	0.8	1114	13	US-10-052-586-271	Sequence 271, A
C 277	22	0.8	645	18	US-10-425-115-102260	Sequence 102260, A	C 350	22	0.8	1114	14	US-10-174-550-271	Sequence 271, A
C 278	22	0.8	645	18	US-10-425-115-34485	Sequence 34485, A	C 351	22	0.8	1114	14	US-10-176-758-271	Sequence 271, A
C 279	22	0.8	647	18	US-10-425-115-95731	Sequence 95731, A	C 352	22	0.8	1114	14	US-10-175-737-271	Sequence 271, A
C 280	22	0.8	648	13	US-10-027-632-83029	Sequence 83029, A	C 353	22	0.8	1114	14	US-10-175-581-271	Sequence 271, A
C 281	22	0.8	648	15	US-10-027-632-83029	Sequence 83029, A	C 354	22	0.8	1114	14	US-10-176-483-271	Sequence 271, A
C 282	22	0.8	658	14	US-10-097-065-131	Sequence 131, A	C 355	22	0.8	1114	14	US-10-176-749-271	Sequence 271, A
C 283	22	0.8	658	15	US-10-372-876-131	Sequence 131, A	C 356	22	0.8	1114	14	US-10-176-914-271	Sequence 271, A
C 284	22	0.8	660	14	US-10-198-846-8749	Sequence 8749, A	C 357	22	0.8	1114	14	US-10-176-915-271	Sequence 271, A
C 285	22	0.8	682	18	US-10-425-115-154557	Sequence 154557, A	C 358	22	0.8	1114	14	US-10-173-706-271	Sequence 271, A
C 286	22	0.8	685	15	US-10-231-417-145	Sequence 145, A	C 359	22	0.8	1114	14	US-10-175-728-271	Sequence 271, A
C 287	22	0.8	685	9	US-09-910-943-288	Sequence 288, A	C 360	22	0.8	1114	14	US-10-175-752-271	Sequence 271, A
C 288	22	0.8	697	17	US-10-437-963-27870	Sequence 27870, A	C 361	22	0.8	1114	14	US-10-176-482-271	Sequence 271, A
C 289	22	0.8	699	17	US-10-767-701-500	Sequence 500, A	C 362	22	0.8	1114	14	US-10-176-757-271	Sequence 271, A
C 290	22	0.8	709	17	US-10-767-701-1302	Sequence 1302, A	C 363	22	0.8	1114	14	US-10-176-913-271	Sequence 271, A
C 291	22	0.8	716	18	US-10-425-115-137609	Sequence 137609, A	C 364	22	0.8	1114	14	US-10-180-552-271	Sequence 271, A
C 292	22	0.8	717	16	US-10-428-681-43	Sequence 43, A	C 365	22	0.8	1114	14	US-10-180-552-271	Sequence 271, A
C 293	22	0.8	718	13	US-10-027-632-98250	Sequence 98250, A	C 366	22	0.8	1114	14	US-10-173-700-271	Sequence 271, A
C 294	22	0.8	718	15	US-10-027-632-98250	Sequence 98250, A	C 367	22	0.8	1114	14	US-10-174-572-271	Sequence 271, A
C 295	22	0.8	726	13	US-10-027-632-18930	Sequence 18930, A	C 368	22	0.8	1114	14	US-10-174-579-271	Sequence 271, A
C 296	22	0.8	726	13	US-10-027-632-18931	Sequence 18931, A	C 369	22	0.8	1114	14	US-10-174-582-271	Sequence 271, A
C 297	22	0.8	726	15	US-10-027-632-18930	Sequence 18930, A	C 370	22	0.8	1114	14	US-10-174-588-271	Sequence 271, A
C 298	22	0.8	726	15	US-10-027-632-18931	Sequence 18931, A	C 371	22	0.8	1114	14	US-10-175-729-271	Sequence 271, A
C 299	22	0.8	737	16	US-10-424-599-92387	Sequence 92387, A	C 372	22	0.8	1114	14	US-10-175-740-271	Sequence 271, A
C 300	22	0.8	740	18	US-10-425-115-18580	Sequence 18580, A	C 373	22	0.8	1114	14	US-10-175-743-271	Sequence 271, A
C 301	22	0.8	741	18	US-10-425-115-14123	Sequence 14123, A	C 374	22	0.8	1114	14	US-10-176-468-271	Sequence 271, A
C 302	22	0.8	747	18	US-10-425-115-145902	Sequence 145902, A	C 375	22	0.8	1114	14	US-10-176-462-271	Sequence 271, A
C 303	22	0.8	763	15	US-10-442-017-24	Sequence 24, A	C 376	22	0.8	1114	14	US-10-176-747-271	Sequence 271, A
C 304	22	0.8	770	13	US-10-027-632-148328	Sequence 148328, A	C 377	22	0.8	1114	14	US-10-176-750-271	Sequence 271, A

670	22	0.8	1114	14	US-10-196-753-271	Sequence 271, App	743	22	0.8	1114	14	US-10-173-693-271	Sequence 271, App
671	22	0.8	1114	14	US-10-196-761-271	Sequence 271, App	744	22	0.8	1114	14	US-10-174-578-271	Sequence 271, App
672	22	0.8	1114	14	US-10-197-652-271	Sequence 271, App	745	22	0.8	1114	14	US-10-175-741-271	Sequence 271, App
673	22	0.8	1114	14	US-10-197-693-271	Sequence 271, App	746	22	0.8	1114	14	US-10-175-750-271	Sequence 271, App
674	22	0.8	1114	14	US-10-197-696-271	Sequence 271, App	747	22	0.8	1114	14	US-10-176-886-271	Sequence 271, App
675	22	0.8	1114	14	US-10-197-698-271	Sequence 271, App	748	22	0.8	1114	14	US-10-184-641-271	Sequence 271, App
676	22	0.8	1114	14	US-10-197-703-271	Sequence 271, App	749	22	0.8	1114	14	US-10-187-888-271	Sequence 271, App
677	22	0.8	1114	14	US-10-197-711-271	Sequence 271, App	750	22	0.8	1114	14	US-10-194-360-271	Sequence 271, App
678	22	0.8	1114	14	US-10-198-751-271	Sequence 271, App	751	22	0.8	1114	14	US-10-194-365-271	Sequence 271, App
679	22	0.8	1114	14	US-10-198-761-271	Sequence 271, App	752	22	0.8	1114	14	US-10-195-895-271	Sequence 271, App
680	22	0.8	1114	14	US-10-198-762-271	Sequence 271, App	753	22	0.8	1114	14	US-10-199-302-271	Sequence 271, App
681	22	0.8	1114	14	US-10-198-763-271	Sequence 271, App	754	22	0.8	1114	14	US-10-201-223-271	Sequence 271, App
682	22	0.8	1114	14	US-10-198-767-271	Sequence 271, App	755	22	0.8	1114	14	US-10-205-610-271	Sequence 271, App
683	22	0.8	1114	14	US-10-199-301-271	Sequence 271, App	756	22	0.8	1114	14	US-10-205-891-271	Sequence 271, App
684	22	0.8	1114	14	US-10-199-307-271	Sequence 271, App	757	22	0.8	1114	14	US-10-206-817-271	Sequence 271, App
685	22	0.8	1114	14	US-10-199-312-271	Sequence 271, App	758	22	0.8	1114	14	US-10-207-923-271	Sequence 271, App
686	22	0.8	1114	14	US-10-199-315-271	Sequence 271, App	759	22	0.8	1114	14	US-10-207-924-271	Sequence 271, App
687	22	0.8	1114	14	US-10-199-316-271	Sequence 271, App	760	22	0.8	1114	14	US-10-208-028-271	Sequence 271, App
688	22	0.8	1114	14	US-10-199-457-271	Sequence 271, App	761	22	0.8	1114	14	US-10-012-121X-110	Sequence 110, App
689	22	0.8	1114	14	US-10-199-459-271	Sequence 271, App	762	22	0.8	1114	14	US-10-205-904-271	Sequence 271, App
690	22	0.8	1114	14	US-10-199-460-271	Sequence 271, App	763	22	0.8	1114	14	US-10-175-753-271	Sequence 271, App
691	22	0.8	1114	14	US-10-199-461-271	Sequence 271, App	764	22	0.8	1114	14	US-10-180-553-271	Sequence 271, App
692	22	0.8	1114	14	US-10-199-667-271	Sequence 271, App	765	22	0.8	1114	14	US-10-201-327-271	Sequence 271, App
693	22	0.8	1114	14	US-10-199-673-271	Sequence 271, App	766	22	0.8	1114	14	US-10-121-062-271	Sequence 271, App
694	22	0.8	1114	14	US-10-201-321-271	Sequence 271, App	767	22	0.8	1114	14	US-10-006-116X-110	Sequence 110, App
695	22	0.8	1114	14	US-10-201-332-271	Sequence 271, App	768	22	0.8	1114	14	US-10-006-117X-110	Sequence 110, App
696	22	0.8	1114	14	US-10-201-336-271	Sequence 271, App	769	22	0.8	1114	14	US-10-017-527X-110	Sequence 110, App
697	22	0.8	1114	14	US-10-201-532-271	Sequence 271, App	770	22	0.8	1114	14	US-10-183-003-271	Sequence 271, App
698	22	0.8	1114	14	US-10-201-533-271	Sequence 271, App	771	22	0.8	1114	14	US-10-183-016-271	Sequence 271, App
699	22	0.8	1114	14	US-10-201-535-271	Sequence 271, App	772	22	0.8	1114	14	US-10-173-696-271	Sequence 271, App
700	22	0.8	1114	14	US-10-201-769-271	Sequence 271, App	773	22	0.8	1114	14	US-10-013-913X-110	Sequence 110, App
701	22	0.8	1114	14	US-10-201-771-271	Sequence 271, App	774	22	0.8	1114	14	US-10-125-823X-271	Sequence 271, App
702	22	0.8	1114	14	US-10-201-854-271	Sequence 271, App	775	22	0.8	1114	14	US-10-176-491-271	Sequence 271, App
703	22	0.8	1114	14	US-10-202-410-271	Sequence 271, App	776	22	0.8	1114	14	US-10-176-979-271	Sequence 271, App
704	22	0.8	1114	14	US-10-202-473-271	Sequence 271, App	777	22	0.8	1114	14	US-10-187-592-271	Sequence 271, App
705	22	0.8	1114	14	US-10-202-474-271	Sequence 271, App	778	22	0.8	1114	14	US-10-007-194X-110	Sequence 110, App
706	22	0.8	1114	14	US-10-205-503-271	Sequence 271, App	779	22	0.8	1114	14	US-10-197-691-271	Sequence 271, App
707	22	0.8	1114	14	US-10-205-512-271	Sequence 271, App	780	22	0.8	1114	14	US-10-198-771-271	Sequence 271, App
708	22	0.8	1114	14	US-10-205-882-271	Sequence 271, App	781	22	0.8	1114	14	US-10-013-430X-110	Sequence 110, App
709	22	0.8	1114	14	US-10-205-894-271	Sequence 271, App	782	22	0.8	1114	14	US-10-174-575X-271	Sequence 271, App
710	22	0.8	1114	14	US-10-205-896-271	Sequence 271, App	783	22	0.8	1114	14	US-10-179-520-271	Sequence 271, App
711	22	0.8	1114	14	US-10-205-898-271	Sequence 271, App	784	22	0.8	1114	14	US-10-201-325-271	Sequence 271, App
712	22	0.8	1114	14	US-10-205-901-271	Sequence 271, App	785	22	0.8	1114	14	US-10-202-941-271	Sequence 271, App
713	22	0.8	1114	14	US-10-205-903-271	Sequence 271, App	786	22	0.8	1114	14	US-10-205-910-271	Sequence 271, App
714	22	0.8	1114	14	US-10-206-909-271	Sequence 271, App	787	22	0.8	1114	14	US-10-011-671X-110	Sequence 110, App
715	22	0.8	1114	14	US-10-206-910-271	Sequence 271, App	788	22	0.8	1114	14	US-10-012-755X-110	Sequence 110, App
716	22	0.8	1114	14	US-10-206-911-271	Sequence 271, App	789	22	0.8	1114	14	US-10-015-386X-110	Sequence 110, App
717	22	0.8	1114	14	US-10-206-912-271	Sequence 271, App	790	22	0.8	1114	15	US-10-179-526-271	Sequence 271, App
718	22	0.8	1114	14	US-10-206-913-271	Sequence 271, App	791	22	0.8	1114	15	US-10-173-701-271	Sequence 271, App
719	22	0.8	1114	14	US-10-206-914-271	Sequence 271, App	792	22	0.8	1114	15	US-10-179-511-271	Sequence 271, App
720	22	0.8	1114	14	US-10-206-920-271	Sequence 271, App	793	22	0.8	1114	15	US-10-179-518-271	Sequence 271, App
721	22	0.8	1114	14	US-10-206-921-271	Sequence 271, App	794	22	0.8	1114	15	US-10-183-018-271	Sequence 271, App
722	22	0.8	1114	14	US-10-206-923-271	Sequence 271, App	795	22	0.8	1114	15	US-10-184-624-271	Sequence 271, App
723	22	0.8	1114	14	US-10-206-925-271	Sequence 271, App	796	22	0.8	1114	15	US-10-184-657-271	Sequence 271, App
724	22	0.8	1114	14	US-10-206-926-271	Sequence 271, App	797	22	0.8	1114	15	US-10-197-701-271	Sequence 271, App
725	22	0.8	1114	14	US-10-206-927-271	Sequence 271, App	798	22	0.8	1114	15	US-10-197-706-271	Sequence 271, App
726	22	0.8	1114	14	US-10-207-916-271	Sequence 271, App	799	22	0.8	1114	15	US-10-201-857-271	Sequence 271, App
727	22	0.8	1114	14	US-10-207-917-271	Sequence 271, App	800	22	0.8	1114	15	US-10-202-813-271	Sequence 271, App
728	22	0.8	1114	14	US-10-207-918-271	Sequence 271, App	801	22	0.8	1114	15	US-10-202-938-271	Sequence 271, App
729	22	0.8	1114	14	US-10-207-919-271	Sequence 271, App	802	22	0.8	1114	15	US-10-202-940-271	Sequence 271, App
730	22	0.8	1114	14	US-10-207-920-271	Sequence 271, App	803	22	0.8	1114	15	US-10-205-508-271	Sequence 271, App
731	22	0.8	1114	14	US-10-207-925-271	Sequence 271, App	804	22	0.8	1114	15	US-10-205-905-271	Sequence 271, App
732	22	0.8	1114	14	US-10-208-021-271	Sequence 271, App	805	22	0.8	1114	15	US-10-206-818-271	Sequence 271, App
733	22	0.8	1114	14	US-10-208-022-271	Sequence 271, App	806	22	0.8	1114	15	US-10-208-025-271	Sequence 271, App
734	22	0.8	1114	14	US-10-208-023-271	Sequence 271, App	807	22	0.8	1114	15	US-10-011-692X-110	Sequence 110, App
735	22	0.8	1114	14	US-10-208-026-271	Sequence 271, App	808	22	0.8	1114	15	US-10-006-768X-110	Sequence 110, App
736	22	0.8	1114	14	US-10-208-029-271	Sequence 271, App	809	22	0.8	1114	15	US-10-017-610X-110	Sequence 110, App
737	22	0.8	1114	14	US-10-208-030-271	Sequence 271, App	810	22	0.8	1114	15	US-10-198-760-271	Sequence 271, App
738	22	0.8	1114	14	US-10-015-393X-110	Sequence 110, App	811	22	0.8	1114	15	US-10-201-772-271	Sequence 271, App
739	22	0.8	1114	14	US-10-232-232-271	Sequence 271, App	812	22	0.8	1114	15	US-10-006-063X-110	Sequence 110, App
740	22	0.8	1114	14	US-10-195-898-271	Sequence 271, App	813	22	0.8	1114	15	US-10-020-063X-110	Sequence 110, App
741	22	0.8	1114	14	US-10-196-759-271	Sequence 271, App	814	22	0.8	1114	15	US-10-184-613-271	Sequence 271, App
742	22	0.8	1114	14	US-10-015-869X-110	Sequence 110, App	815	22	0.8	1114	15	US-10-187-739-271	Sequence 271, App

816	22	0.8	1114	15	US-10-206-907-271	Sequence 271, App	889	22	0.8	1114	15	US-10-013-911A-110	Sequence 110, App
817	22	0.8	1114	15	US-10-015-391A-110	Sequence 110, App	890	22	0.8	1114	15	US-10-013-912A-110	Sequence 110, App
818	22	0.8	1114	15	US-10-183-009-271	Sequence 271, App	891	22	0.8	1114	15	US-10-015-653A-110	Sequence 110, App
819	22	0.8	1114	15	US-10-187-755-271	Sequence 271, App	892	22	0.8	1114	15	US-10-012-101B-110	Sequence 110, App
820	22	0.8	1114	15	US-10-017-407A-110	Sequence 110, App	893	22	0.8	1114	15	US-10-015-480A-110	Sequence 110, App
821	22	0.8	1114	15	US-10-011-833A-110	Sequence 110, App	894	22	0.8	1114	15	US-10-015-715A-110	Sequence 110, App
822	22	0.8	1114	15	US-10-006-041A-110	Sequence 110, App	895	22	0.8	1114	15	US-10-012-237A-110	Sequence 110, App
823	22	0.8	1114	15	US-10-015-822A-110	Sequence 110, App	896	22	0.8	1114	15	US-10-013-906A-110	Sequence 110, App
824	22	0.8	1114	15	US-10-015-387A-110	Sequence 110, App	897	22	0.8	1114	15	US-10-015-388A-110	Sequence 110, App
825	22	0.8	1114	15	US-10-006-130A-110	Sequence 110, App	898	22	0.8	1114	15	US-10-012-753A-110	Sequence 110, App
826	22	0.8	1114	15	US-10-199-672-271	Sequence 271, App	899	22	0.8	1114	15	US-10-015-385A-110	Sequence 110, App
827	22	0.8	1114	15	US-10-006-172A-110	Sequence 110, App	900	22	0.8	1114	15	US-10-007-236A-110	Sequence 110, App
828	22	0.8	1114	15	US-10-187-749-271	Sequence 271, App	901	22	0.8	1114	15	US-10-015-389A-110	Sequence 110, App
829	22	0.8	1114	15	US-10-194-457-271	Sequence 271, App	902	22	0.8	1114	15	US-10-015-519A-110	Sequence 110, App
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831	22	0.8	1114	15	US-10-196-747-271	Sequence 271, App	904	22	0.8	1114	15	US-10-013-915A-110	Sequence 110, App
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 983 22 0.8 1982 18 US-10-733-930-1030 Sequence 1030, Ap
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ALIGNMENTS

RESULT 1
 US-09-780-525-1
 ; Sequence 1, Application US/09780525
 ; Patent No. US20020004223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bin-Bing Zhou
 ; APPLICANT: Yuan Zhu
 ; APPLICANT: Priya Chaturvedi
 ; APPLICANT: Mark R. Hurle
 ; APPLICANT: Xiaolong Li
 ; TITLE OF INVENTION: FHARL, A NEW RING FINGER PROTEIN
 ; FILE REFERENCE: GP-70668-C1
 ; CURRENT APPLICATION NUMBER: US/09/780,525
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 09/456,876
 ; PRIOR FILING DATE: 1999-12-08
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1995
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 ; US-09-780-525-1

Query Match 74.5%; Score 1995; DB 9; Length 1995;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2073, Application US/10108260A			
; Publication No. US20040005560A1			
; GENERAL INFORMATION:			
; APPLICANT: HELIX RESEARCH INSTITUTE			
; TITLE OF INVENTION: No. US20040005560A1el full length cdna			
; FILE REFERENCE: HI-A0106			
; CURRENT APPLICATION NUMBER: US/10/108, 260A			
; CURRENT FILING DATE: 2002-03-27			

Query Match	Best Local Similarity	Score	DB	Length
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Qy	1368	CGTGGCCGCGAGTGTCTCTGAGTACAGAGGCAAGCGCGGCGGACCTCCCACTGCGCAGC	1427	
Db	1017	CGTGGCCGCGAGTGTCTCTGAGTACAGAGGCAAGCGCGGCGGACCTCCCACTGCGCAGC	1076	
Qy	1428	ACCCGAGGCGAGCCAGAGAGCCCAACAGGCTCTGGGGATGACACCTTCAAGTCCGTGAG	1487	
Db	1077	ACCCGAGGCGAGCCAGAGAGCCCAACAGGCTCTGGGGATGACACCTTCAAGTCCGTGAG	1136	
Qy	1488	CTTGAACAGCAGAGTCCAGATTACGTGTGCTCTGACAGAAAGCCACGCTGTGAC	1547	
Db	1137	CTTGAACAGCAGAGTCCAGATTACGTGTGCTCTGACAGAAAGCCACGCTGTGAC	1196	
Qy	1548	CTGCTGCTTCCAGGCGCAATGCCGACGGAGAGTGAAGGCGGAGAGACCCGCGTGTGCG	1607	
Db	1197	CTGCTGCTTCCAGGCGCAATGCCGACGGAGAGTGAAGGCGGAGAGACCCGCGTGTGCG	1256	
Qy	1608	CCCTCAGACAGTGTGCTGCTGCTGACAGCTTTTCTGCACTCTTATCTGAGGCTGCAACCG	1667	

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Db      1257 CCTCAGCAGTGTGGCTGTGCTGACGCTTTCGCACTGTACTGGGGCTGCACCCG 1316
Qy      1668 GACCGGCTCTAGCGGCTGCTGACCCCGCTTTGTG 1702
Db      1317 GACCGGCTCTAGCGGCTGCTGACCCCGCTTTGTG 1351

RESULT 3
US-09-764-864-22
; Sequence 22, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1281)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-22

Query Match      28.6%; Score 765; DB 9; Length 1311;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      710 GGTCTGGGGGGTGGTGGCATCTCCCTAAAGAAAGAGTGTCCCTGTGGCAAGTGAAG 769
Db      383 GGTCTGGGGGGTGGTGGCATCTCCCTAAAGAAAGTGTCCCTGTGGCAAGTGAAG 442
Qy      770 TCTCCAGCTTGTGCTCAGCTCTCCAGACAGAAAGACTGCTCTTTTGTGCTGGAAAC 829
Db      443 TCTCCAGCTTGTGCTCAGCTCTCCAGACAGAAAGACTGCTCTTTTGTGCTGGAAAC 502
Qy      830 CCCAGGATCAGAGAGATTGAGAGCCCGTGAAGAAATGAGAGAGATGGGACCTTG 889
Db      503 CCCAGGATCAGAGAGATTGAGAGCCCGTGAAGAAATGAGAGAGATGGGACCTTG 562
Qy      890 ACCGTGAACGGGAGATTGTTGTGTGCAACAACCGGTGAATGCCCCAAACCGTCCAGAG 949
Db      563 ACCGTGAACGGGAGATTGTTGTGTGCAACAACCGGTGAATGCCCCAAACCGTCCAGAG 622
Qy      950 AGCTCAGACAGCGGCTGGGAAACAGACAAAGATGAGAGAGAGCTGACATGATCATCT 1009
Db      623 AGCTCAGACAGCGGCTGGGAAACAGACAAAGATGAGAGAGAGCTGACATGATCATCT 682
Qy      1010 GCCAGAGCTGCTGCAACGACTGCTGATTTGAGAGCCCTGTCATGCAAGTTTGTGCGCG 1069
Db      683 GCCAGAGCTGCTGCAACGACTGCTGATTTGAGAGCCCTGTCATGCAAGTTTGTGCGCG 742
Qy      1070 CTGTGCTACTCGGGCTGAGATGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129
Db      743 CTGTGCTACTCGGGCTGAGATGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 802
Qy      1130 AGCGAGTCTGTAAACCAACATCTCTCAACAACCTGTGAGAGCATCTCATCAGACATC 1189
Db      803 AGCGAGTCTGTAAACCAACATCTCTCAACAACCTGTGAGAGCATCTCATCAGACATC 862
Qy      1190 CAGACAAAGTGGCAAGTGAAGAGATGTGCAAAAGTATGATGTCAGAGAAATAAATCACTC 1249
Db      863 CAGACAAAGTGGCAAGTGAAGAGATGTGCAAAAGTATGATGTCAGAGAAATAAATCACTC 922
Qy      1250 AAGACATGCTGCAGCCCAAGTCAAGGCGGTCTTTTCTGATGAAGAGGAGTTGAGAG 1309

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Db      923 AAGACATGCTGCAGCCCAAGTCAAGCGGTCTTTTCTGATGAAGAGAGATTCAAGG 982
Qy      1310 ACTGTCTGAGCTGTGACAGCTTGAAGTGTCTTCAAGATTGACCAAGCATACGTG 1369
Db      983 ACTGTCTGAGCTGTGACAGCTTGAAGTGTCTTCAAGATTGACCAAGCATACGTG 1042
Qy      1370 TGTGCGGCGAGTGTCTGATGAAGAGAGCGGGGCGAGCTGCCCATGCGCAGAGC 1429
Db      1043 TGTGCGGCGAGTGTCTGATGAAGAGAGCGGGGCGAGCTGCCCATGCGCAGAGC 1102
Qy      1430 CCGAGGCGGAGCCAGAGAGCCCAAGGCGCTGTGGGGATGACACCT 1474
Db      1103 CCGAGGCGGAGCCAGAGAGCCCAAGGCGCTGTGGGGATGACACCT 1147

RESULT 4
US-10-094-749-160
; Sequence 160, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUYI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUDKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-160

Query Match      23.6%; Score 633; DB 15; Length 2186;
Best Local Similarity 99.7%; Pred. No. 2,7e-310;
Matches 863; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy      1796 TGACATGAAAAAATGTTGACCGAGAGCTGTGAGCTCTCCAGCGGGAGTGTTCCTG 1855
Db      695 TGACATGAAAAAATGTTGACCGAGAGCTGTGAGCTCTCCAGCGGGAGTGTTCCTG 754
Qy      1856 TGTCTGATTAAGAGATCAAGGAGACACCTTCTGTGTTACGTCGTGGCCCGCAGCT 1915
Db      755 TGTCTGATTAAGAGATCAAGGAGACACCTTCTGTGTTACGTCGTGGCCCGCAGCT 814
Qy      1916 TCCGTGAGTCACTATCAAGTATCGGAGAAACATTCCTGCTCCAGAGTTGCCAGTGGCCG 1975
Db      815 TCCGTGAGTCACTATCAAGTATCGGAGAAACATTCCTGCTCCAGAGTTGCCAGTGGCCG 874
Qy      1976 TAAACATCCCGTCTGACTGCTACTGAGGCGGTAACTCCGCACTAGAGTGAAGCTCACC 2035
Db      875 TAAACATCCCGTCTGACTGCTACTGAGGCGGTAACTCCGCACTAGAGTGAAGCTCACC 934

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; LOCATION: (300)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-322

Query Match
Best Local Similarity 100.0%; Score 267; DB 9; Length 357;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 TCCGGGTTTCGGCGCGGGGAGTGAATCCCGATGAGCGGCCCGAGGAAGGCAAC 115
DB 5 TCCGGGTTTCGGCGCGGGGAGTGAATCCCGATGAGCGGCCCGAGGAAGGCAAC 64
QY 116 AGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 175
DB 65 AGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 124
QY 176 CGCAGCTCTCTCTGAGAGAGCGGAGTGAACATCGGCGGAGAGAGAGGTTGCGACCTT 235
DB 125 CGCAGCTCTCTCTGAGAGAGCGGAGTGAACATCGGCGGAGAGAGAGGTTGCGACCTT 184
QY 236 CCTTCCCGAGCAATAAAGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAAT 295
DB 185 CCTTCCCGAGCAATAAAGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAAT 244
QY 296 CAGTCAGGTGACACTGGAAGATACCA 322
DB 245 CAGTCAGGTGACACTGGAAGATACCA 271

RESULT 7
US-09-764-864-323
; Sequence 323, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 323
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (313)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-323

Query Match
Best Local Similarity 8.9%; Score 238; DB 9; Length 354;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GCAATTAACGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAATCAGGTCAGG 304
DB 51 GCAATTAACGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAATCAGGTCAGG 110
QY 305 TGACACTGGAAGATACCAAGCAGCAGTGAACAGTGAATTAACAAGCTGAAGGTTGTAAGA 364
DB 111 TGACACTGGAAGATACCAAGCAGCAGTGAACAGTGAATTAACAAGCTGAAGGTTGTAAGA 170
QY 365 AGCAGACATGCGCTTACAGACTGGGAGTGCATCTATGAACTTTAAGTGAAGCAAGCATGACACA 424
DB 171 AGCAGACATGCGCTTACAGACTGGGAGTGCATCTATGAACTTTAAGTGAAGCAAGCATGACACA 230
QY 425 CGGAACACACGTGGCATACCTTATGAATCTTTAAGTGAAGCAAGCATGACACA 482
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DB 231 CGGAACACACGTGGCATACCTTATGAATCTTTAAGTGAAGCAAGCATGACACA 288

RESULT 8
US-09-764-864-742
; Sequence 742, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 742
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (313)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-742

Query Match
Best Local Similarity 8.9%; Score 238; DB 9; Length 354;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GCAATTAACGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAATCAGGTCAGG 304
DB 51 GCAATTAACGTGTCTCTGAGATCACTGTAAGATTGATGATGAATAATCAGGTCAGG 110
QY 305 TGACACTGGAAGATACCAAGCAGCAGTGAACAGTGAATTAACAAGCTGAAGGTTGTAAGA 364
DB 111 TGACACTGGAAGATACCAAGCAGCAGTGAACAGTGAATTAACAAGCTGAAGGTTGTAAGA 170
QY 365 AGCAGACATGCGCTTACAGACTGGGAGTGCATCTATGAACTTTAAGTGAAGCAAGCATGACACA 424
DB 171 AGCAGACATGCGCTTACAGACTGGGAGTGCATCTATGAACTTTAAGTGAAGCAAGCATGACACA 230
QY 425 CGGAACACACGTGGCATACCTTATGAATCTTTAAGTGAAGCAAGCATGACACA 482
DB 231 CGGAACACACGTGGCATACCTTATGAATCTTTAAGTGAAGCAAGCATGACACA 288

RESULT 9
US-09-918-995-13662
; Sequence 13662, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13662
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
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US-09-918-995-13662

Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-99;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2445 AGTTTAAAGGAGAGAGGCAAGTTTCAAAAACATTTGTTTCAGAGAGGAGCATTAAG 2504

DB 92 AGTTTCAAGGAGAGAGGCAAGTTTCAAAAACATTTGTTTCAGAGAGGAGCATTAAG 151

QY 2505 TTTACAGCTTACAGAGAGTACACAAATTCCTGCTGGGAAAACACAGCATTTATCT 2564

DB 152 TTTACAGCTTACAGAGAGTACACAAATTCCTGCTGGGAAAACACAGCATTTATCT 211

QY 2565 ATTTTATTTATTAAGTTTGGTGTATCTCTATTAAGTTTAAAGTCAAACTG 2624

DB 212 ATTTTATTTATTAAGTTTGGTGTATCTCTATTAAGTTTAAAGTCAAACTG 271

QY 2625 TAGCACAATAATATTAATTTATTAATTTCAAAATTGAC 2661

DB 272 TAGCACAATAATATTAATTTATTAATTTCAAAATTGAC 308

RESULT 10

US-09-918-995-2180
; Sequence 2180, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:

; APPLICANT: HySeq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; PRIOR FILING DATE: 2001-07-30

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2180

; LENGTH: 476

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(476)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-2180

Query Match

Best Local Similarity 2.9%; Score 77; DB 10; Length 476;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 ATTCAATCATATCTGTGAACAGCAAGTTCAAAAACATTAAGATTCAGAGCCCTGAGCA 2105

DB 52 ATTCAATCATATCTGTGAACAGCAAGTTCAAAAACATTAAGATTCAGAGCCCTGAGCA 111

QY 2106 GCTTTACAGCACTGAGG 2122

DB 112 GCTTTACAGCACTGAGG 128

RESULT 11

US-09-908-975-6220
; Sequence 6220, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: FAIGER, Simcha

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICER

; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME

FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6220
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-908-975-6220

Query Match

Best Local Similarity 2.2%; Score 60; DB 10; Length 60;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1843 GGAGTGTCTGCTGTGATTACAGAGTCAGGAGACACCGTCTGTACTGCTGT 1902

DB 1 GGAGTGTCTGCTGTGATTACAGAGTCAGGAGACACCGTCTGTACTGCTGT 60

RESULT 12

US-10-425-115-112922/c
; Sequence 112922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 112922

; LENGTH: 281

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_34473C.1

US-10-425-115-112922

Query Match

Best Local Similarity 1.0%; Score 26; DB 18; Length 281;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2654 AAATTGACAAAAA 2679

DB 43 AAATTGACAAAAA 18

RESULT 13

US-10-719-993-23863/c
; Sequence 23863, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001496

; CURRENT APPLICATION NUMBER: US/10/719,993

; CURRENT FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 55342

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23863

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-719-993-23863

Query Match 0.9%; Score 25; DB 18; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAAAAAAAAAAAAAAAAA 2679

DB 26 AATTGACAAAAAAAAAAAAAAAAAAAA 2

RESULT 14

US-10-304-928-15
; Sequence 15, Application US/10304928
; Publication No. US20030101484A1
; GENERAL INFORMATION:
; APPLICANT: Yalpani, Nasser
; APPLICANT: Yalpani, Carl R.
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; FILE REFERENCE: 1100D
; CURRENT APPLICATION NUMBER: US/10/304,928
; PRIOR APPLICATION NUMBER: 09/522,714
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/125,915
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1085
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)...(966)
US-10-304-928-15

Query Match 0.9%; Score 25; DB 15; Length 1085;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAAAAAAAAAAAAAAAAA 2679

DB 1061 AATTGACAAAAAAAAAAAAAAAAAAAA 1085

RESULT 15

US-10-425-115-124808
; Sequence 124808, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 124808
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_45300C.1
US-10-425-115-124808

Query Match 0.9%; Score 25; DB 18; Length 1253;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAAAAAAAAAAAAAAAAA 2679
DB 1197 AATTGACAAAAAAAAAAAAAAAAAAAA 1221

RESULT 16

US-09-957-664-1
; Sequence 1, Application US/09957664
; Patent No. US20020123097A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 63760, A NOVEL HUMAN TRANSPORTER AND
; FILE REFERENCE: MNI-192
; CURRENT APPLICATION NUMBER: US/09/957,664
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,790
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(1491)
US-09-957-664-1

Query Match 0.9%; Score 25; DB 9; Length 1963;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAAAAAAAAAAAAAAAAA 2679

DB 1916 AATTGACAAAAAAAAAAAAAAAAAAAA 1940

RESULT 17

US-10-154-419-15
; Sequence 15, Application US/10154419
; Publication No. US20030143675A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Gluckman, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,
; TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
; TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALFL, FBH58295FL, 57255,
; TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-249
; CURRENT APPLICATION NUMBER: US/10/154,419
; CURRENT FILING DATE: 2002-05-22
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq Version 4.0
; SEQ ID NO 15
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(1491)
US-10-154-419-15

Query Match 0.9%; Score 25; DB 15; Length 1963;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2655 AATTGACAAAAAAAAAAAAAAAAAAAA 2679

DB 1916 AATTGACAAAAAAAAAAAAAAAAAAAA 1940


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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (219)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-846-50

Query Match          0.9%; Score 24; DB 9; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB      145 ATTGACCAAAAAAAAAAAAAAAAA 168

RESULT 23
US-09-764-846-122
; Sequence 122, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 122
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (219)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-846-122

Query Match          0.9%; Score 24; DB 9; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB      145 ATTGACCAAAAAAAAAAAAAAAAA 168

RESULT 24
US-10-091-483-50
; Sequence 50, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
```

```
; SEQ ID NO 50
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)_feature
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (219)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-483-50

Query Match          0.9%; Score 24; DB 14; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB      145 ATTGACCAAAAAAAAAAAAAAAAA 168

RESULT 25
US-10-091-483-122
; Sequence 122, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 122
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)_feature
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (219)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-483-122

Query Match          0.9%; Score 24; DB 14; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB      145 ATTGACCAAAAAAAAAAAAAAAAA 168

RESULT 26
US-10-357-930-20027
; Sequence 20027, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endegge, Wilison
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
```

```
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20027
/ LENGTH: 291
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..2..4
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20027
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 291;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB 199 ATTGACCAAAAAAAAAAAAAAAAA 222
```

```
RESULT 27
US-10-242-535A-21114
/ Sequence 21114, Application US/10242535A
/ Publication No. US20040013663A1
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: liew, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2005
/ CURRENT APPLICATION NUMBER: US/10/242,535A
/ CURRENT FILING DATE: 2002-09-12
/ PRIOR APPLICATION NUMBER: US 10/085,783
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 21114
/ LENGTH: 320
/ TYPE: DNA
/ ORGANISM: Human
US-10-242-535A-21114
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 16; Length 320;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB 289 ATTGACCAAAAAAAAAAAAAAAAA 312
```

```
RESULT 28
US-10-085-783A-21114
/ Sequence 21114, Application US/10085783A
/ Publication No. US20040037841A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: liew, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2002
/ CURRENT APPLICATION NUMBER: US/10/085,783A
/ CURRENT FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 21114
/ LENGTH: 320
/ TYPE: DNA
/ ORGANISM: Human
US-10-085-783A-21114
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 16; Length 320;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACCAAAAAAAAAAAAAAAAA 2679
DB 289 ATTGACCAAAAAAAAAAAAAAAAA 312
```

```
RESULT 29
US-10-357-930-49814
/ Sequence 49814, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49814
/ LENGTH: 413
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 328..329..330..331..332..333..334..335..336..349..350..351
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-49814
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 413;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2656 ATTGACAAAAA 2679
 Db 224 ATTGACAAAAA 247

RESULT 30

US-09-918-995-10672
 ; Sequence 10672, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HySeq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10672
 ; LENGTH: 474
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(474)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-918-995-10672

Query Match 0.9%; Score 24; DB 10; Length 474;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2656 ATTGACAAAAA 2679
 Db 449 ATTGACAAAAA 472

RESULT 31

US-10-357-930-60931/c
 ; Sequence 60931, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 60931
 ; LENGTH: 525
 ; TYPE: DNA

; ORGANISM: Homo sapiens
 ; US-10-357-930-60931

Query Match 0.9%; Score 24; DB 18; Length 525;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2656 ATTGACAAAAA 2679
 Db 35 ATTGACAAAAA 12

RESULT 32

US-10-425-115-129128
 ; Sequence 129128, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovall, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 129128
 ; LENGTH: 566
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MFT4577_49238C.1
 ; US-10-425-115-129128

Query Match 0.9%; Score 24; DB 18; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2654 AAATTGACAAAAA 2677
 Db 85 AAATTGACAAAAA 108

RESULT 33

US-10-027-632-147186/c
 ; Sequence 147186, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 147186
 ; LENGTH: 635

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-147186

Query Match
Best Local Similarity 100.0%; Score 24; DB 13; Length 635;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 CCTCCCGAGAGCCCGGGGGCGG 2283
DB 315 CCTCCCGAGAGCCCGGGGGCGG 292

RESULT 34
US-10-027-632-147186/c
; Sequence 147186, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147186
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-147186

Query Match
Best Local Similarity 100.0%; Score 24; DB 15; Length 635;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 CCTCCCGAGAGCCCGGGGGCGG 2283
DB 315 CCTCCCGAGAGCCCGGGGGCGG 292

RESULT 35
US-10-425-115-124214
; Sequence 124214, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2000-02-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124214
; LENGTH: 677
; TYPE: DNA
```

```

; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44763C.1
US-10-425-115-124214

Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 677;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 647 ATTGACAAAAA 670

RESULT 36
US-10-425-115-114433
; Sequence 114433, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2000-02-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114433
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_35847C.1
US-10-425-115-114433

Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 688;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 652 ATTGACAAAAA 675

RESULT 37
US-09-969-034-1012/c
; Sequence 1012, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Aetle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Divedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthachal
; APPLICANT: Lewis, Marcia B.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2001-03-27, 271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1012
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

NAME/KEY: misc feature
LOCATION: 155, 257, 315, 326, 374, 379, 403, 405, 432, 442, 447, 480,
LOCATION: 450, 492, 494, 497, 515, 518, 523, 556, 562, 563, 568, 593,
LOCATION: 601, 607, 612, 613, 626, 627, 631, 634, 638, 641, 645, 654,
LOCATION: 662, 672, 677, 696, 697, 703
OTHER INFORMATION: n = A,T,C or G
US-09-969-034-1012

Query Match 0.9%; Score 24; DB 11; Length 703;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 36 ATTGACAAAAA 13

RESULT 38
US-10-437-963-69278/C
Sequence 69278, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 69278
LENGTH: 724
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_69962C.1
US-10-437-963-69278

Query Match 0.9%; Score 24; DB 17; Length 724;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 65 ATTGACAAAAA 42

RESULT 39
US-10-444-795B-796
Sequence 796, Application US/10444795B
Publication No. US2004007754A1
GENERAL INFORMATION:
APPLICANT: Klinghoffer, Richard
APPLICANT: Lewis, Stephen Patrick
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
FILE REFERENCE: 200125,449
CURRENT APPLICATION NUMBER: US/10/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 796
LENGTH: 844
TYPE: DNA
ORGANISM: Homo sapiens
US-10-444-795B-796

Query Match 0.9%; Score 24; DB 16; Length 844;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 821 ATTGACAAAAA 844

RESULT 40
US-10-723-860-5727
Sequence 5727, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Gineburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882,0193.NFUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 5727
LENGTH: 1486
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-5727

Query Match 0.9%; Score 24; DB 18; Length 1486;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2656 ATTGACAAAAA 2679
DB 884 ATTGACAAAAA 907

RESULT 41
US-10-739-930-5455/C
Sequence 5455, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5455
LENGTH: 1930
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: TRIAR-23APR03-CLUSTER33891_1
US-10-739-930-5455

Query Match 0.9%; Score 24; DB 18; Length 1930;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2654 AAATTGACAAAAA 2677
DB 24 AAATTGACAAAAA 1

RESULT 42
US-10-425-115-119660
Sequence 119660, Application US/10425115

```
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 119860
LENGTH: 2192
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_40795C.1
US-10-425-115-119860

Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 2192;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2656 ATTGACAAAAA 2679
2125 ATTGACAAAAA 2148

RESULT 43
US-09-764-869-2292
Sequence 2292, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2292
LENGTH: 11869
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-869-2292

Query Match
Best Local Similarity 100.0%; Score 24; DB 9; Length 11869;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2260 CCCTCCCAAGAGCCCGGGGCGG 2283
1242 CCCTCCCAAGAGCCCGGGGCGG 1265

RESULT 44
US-10-091-504-2292
Sequence 2292, Application US/10091504
Publication No. US20030059908A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
Prior application removed - See file wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2292
LENGTH: 11869
TYPE: DNA
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ORGANISM: Homo sapiens
US-10-091-504-2292

Query Match
Best Local Similarity 100.0%; Score 24; DB 14; Length 11869;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2260 CCCTCCCAAGAGCCCGGGGCGG 2283
1242 CCCTCCCAAGAGCCCGGGGCGG 1265

RESULT 45
US-10-227-577-2292
Sequence 2292, Application US/10227577
Publication No. US20040005575A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C2
CURRENT APPLICATION NUMBER: US/10/227,577
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/091,504
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2292
LENGTH: 11869
TYPE: DNA
ORGANISM: Homo sapiens
US-10-227-577-2292

Query Match
Best Local Similarity 100.0%; Score 24; DB 16; Length 11869;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2260 CCCTCCCAAGAGCCCGGGGCGG 2283
1242 CCCTCCCAAGAGCCCGGGGCGG 1265

RESULT 46
US-10-292-798-1095/C
Sequence 1095, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
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PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1095
LENGTH: 358246
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(358246)
NAME/KEY: CDS
LOCATION: (201)..(326)
FEATURE:
NAME/KEY: CDS
LOCATION: (605)..(1294)
FEATURE:
NAME/KEY: CDS
LOCATION: (29165)..(29206)
FEATURE:
NAME/KEY: CDS
LOCATION: (39051)..(39221)
FEATURE:
NAME/KEY: CDS
LOCATION: (72539)..(72763)
FEATURE:
NAME/KEY: CDS
LOCATION: (133049)..(133353)
FEATURE:
NAME/KEY: CDS
LOCATION: (261460)..(261526)
FEATURE:
NAME/KEY: CDS
LOCATION: (291173)..(291325)
FEATURE:
NAME/KEY: CDS
LOCATION: (291513)..(291770)
FEATURE:
NAME/KEY: CDS
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FEATURE:
NAME/KEY: CDS
LOCATION: (325058)..(325316)
FEATURE:
NAME/KEY: CDS
LOCATION: (330441)..(330609)
FEATURE:
NAME/KEY: CDS
LOCATION: (337750)..(337828)
FEATURE:
NAME/KEY: CDS
LOCATION: (343822)..(344071)
FEATURE:
NAME/KEY: CDS
LOCATION: (358008)..(358046)
FEATURE:
NAME/KEY: modified_base
LOCATION: (547)..(646)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1659)..(1758)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (2818)..(2917)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

LOCATION: (17179)..(17278)
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FEATURE:
NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
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LOCATION: (64360)..(64459)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (71021)..(71120)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (77979)..(78078)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (81210)..(81309)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (103441)..(103540)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (130963)..(130964)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (130979)..(130979)
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FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (130987)..(130987)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (130997)..(130999)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131002)..(131002)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131019)..(131020)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131022)..(131022)

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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131025)..(131025)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131031)..(131031)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131034)..(131034)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131048)..(131049)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131059)..(131060)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131063)..(131063)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131065)..(131065)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131070)..(131070)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131090)..(131091)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131127)..(131129)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

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Query Match      0.9%; Score 24; DB 15; Length 358246;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2656 ATTGACAAAAA 2679
DB      242855 ATTGACAAAAA 242832

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RESULT 47
US-10-242-535A-54104
; Sequence 54104, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54104
; LENGTH: 160
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-54104

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Query Match      0.9%; Score 23; DB 16; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2657 TTGACAAAAA 2679
DB      130 TTGACAAAAA 152

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RESULT 48
US-10-085-783A-54104
; Sequence 54104, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54104
; LENGTH: 160
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-54104

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Query Match      0.9%; Score 23; DB 16; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2657 TTGACAAAAA 2679
DB      130 TTGACAAAAA 152

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RESULT 49
US-10-741-601-22073/C
; Sequence 22073, Application US/10741601
; Publication No. US2004016519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22073
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-22073

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Query Match      0.9%; Score 23; DB 17; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2657 TTGACAAAAAAAAAAAAAAAA 2679
Db 106 TTGACAAAAAAAAAAAAAAAA 84

RESULT 50

US-09-867-701-9978
; Sequence 9978, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9978
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9978

Query Match 0.9%; Score 23; DB 9; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2657 TTGACAAAAAAAAAAAAAAAA 2679
Db 177 TTGACAAAAAAAAAAAAAAAA 199

Search completed: January 15, 2005, 12:52:34
Job time : 1458 secs